

# JOURNAL OF CREATION

Vol. 30(2) 2016

ISSN 1036-2916

CREATION.com

*PLUTO'S MOONS A  
BIG SURPRISE*

*EVOLUTION OF  
GENE REGULATION  
IMPOSSIBLE*



**THE ICE AGE:**  
*MECHANISM FOR POST  
FLOOD DISPERSAL?*

**THE GENESIS FLOOD:**  
*GENETIC EFFECTS OF  
POPULATION BOTTLENECK*

ORIGINS OF  
**PATHOGENIC  
BACTERIA**



# JOURNAL OF CREATION

An international journal devoted to the presentation and discussion of technical aspects of the sciences such as geology, biology, astronomy, etc., and also geography, archaeology, biblical history, philosophy, etc., as they relate to the study of biblical creation and Noah's Flood.

**COVER:** Artistic impression of a bacterial cell

**IMAGE:** © ralwel/depositphotos.com

## SUBSCRIPTION INFORMATION

### AUSTRALIA

*Creation Ministries International*  
P.O. Box 4545,  
Eight Mile Plains QLD 4113, Australia  
Phone: (07) 3340 9888  
Fax: (07) 3340 9889  
Subscription: A\$39 (3 issues)

### CANADA

*Creation Ministries International*  
300 Mill St, Unit 7, Kitchener, ON  
N2M 5G8  
Phone: (519) 746 7616  
Fax: (519) 746 7617  
Subscriptions and orders only:  
**1-888-251-5360**  
Subscription: C\$39 (3 issues)

### NEW ZEALAND

*Creation Ministries International*  
P.O. Box 39005, Howick,  
Auckland 2145, New Zealand  
Phone and fax: (09) 537 4818  
Subscription: NZ\$59 (3 issues)

### SINGAPORE

*Creation Ministries International*  
P.O. Box 195, 911207, Singapore  
Phone and fax: (65) 9698 4292  
Subscription: S\$50 (3 issues)

### SOUTH AFRICA

*Creation Ministries International*  
P.O. Box 3349,  
Durbanville 7551, South Africa  
Phone: (021) 979 0107  
Fax: (086) 519 0555  
Subscription: R320 (3 issues)

### UK and EUROPE

*Creation Ministries International*  
15 Station Street  
Whetstone  
Leicestershire, LE8 6JS  
United Kingdom  
Phone: (44) 0116 2848 999  
(To email use web 'contact us' form)  
Subscription: £25 (3 issues)

### USA

*Creation Ministries International*  
P.O. Box 350,  
Powder Springs, GA 30127, USA.  
Phone: (800) 6161-CMI  
Fax: (770) 439 9784  
Subscription: US\$39 (3 issues)

### OTHER COUNTRIES

*Creation Ministries International*  
P.O. Box 4545,  
Eight Mile Plains QLD 4113, Australia  
Phone: (+617) 3340 9888  
Fax: (+617) 3340 9889  
Subscription: A\$46 (3 issues):  
Please remit in Australian dollars or  
advise MasterCard or Visa card details

**CREATION.com**

**Printed in Australia,**

**Published by:**

*Creation Ministries International Ltd*

ABN 31 010 120 304

Editorial correspondence should  
be addressed to:

### The Editor

*Journal of Creation*  
*Creation Ministries International*  
PO Box 4545  
Eight Mile Plains  
QLD 4113  
AUSTRALIA

Email: [journal@creation.info](mailto:journal@creation.info)

### Editorial Team

Dr Pierre Jerlström (head)  
Dr Don Batten  
Shaun Doyle  
Dr Ron Neller  
Dr Jonathan Sarfati  
Dr Tas Walker

### Production and Design

Tim Kneipp

### Assistance and/or Sub-editing

Russell Grigg



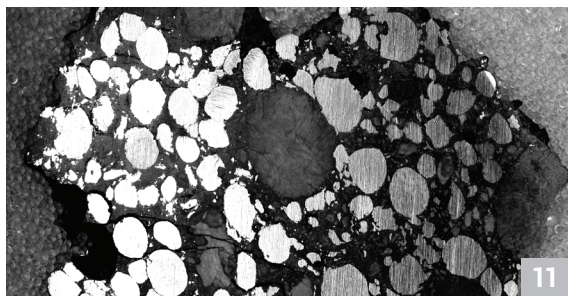
**Worldwide Outreach**

*Creation Ministries International* (CMI)—formerly *Answers in Genesis* in Australia, Canada, New Zealand, Singapore, South Africa and UK/Europe—is a non-profit evangelical group of ministries around the world which, though independent, form an operational unity. We share not only this *Journal of Creation* and the associated *Creation* family magazine, but the same biblical platform, and overall outreach and educational vision. In addition, we communicate and co-operate with bona-fide creationist researchers from all over the world. The expanding effectiveness of these ministries, and the future of quality biblical creation research in general, depends on donations from concerned individuals. These may be made to the CMI office in your country. For other countries, our Australian office is able to receive personal cheques in your own currency, or simply write, phone or fax with your MasterCard or Visa details (including expiry date and amount). We are a fully audited ministry.



## PERSPECTIVES

- 3** How may the presence of mantle water be interpreted?  
» Michael J. Oard
- 4** The fruit of sin vs the fruit of sanctification: a Pauline allusion to Genesis 3 in Romans 6  
» Lita Cosner
- 6** *Samotherium* fossils and variation in the neck within the giraffe kind (Giraffidae)  
» Jean K. Lightner
- 8** Pluto's moons a big surprise!  
» John G. Hartnett
- 9** The uniformitarian puzzle of mountain top planation surfaces  
» Michael J. Oard
- 11** The origin of meteorite chondrules  
» Michael J. Oard
- 12** Changing-look quasars—how do they fit into a biblical creationist model?  
» John G. Hartnett



Chondrites are a mystery for astronomy but their origin is better explained by a recent solar system creation.

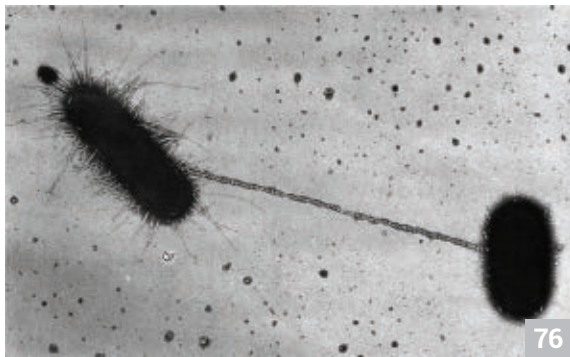
## BOOK REVIEWS

- 15** Vitalism dusted-off as a 'solution' to evolution's fatal problems  
» John Woodmorappe  
» *Evolution 2.0: Breaking the Deadlock Between Darwin and Design* (Perry Marshall)
- 20** Justifying Christian belief  
» Lita Cosner  
» *Apologetics: A Justification of Christian Belief* (John M. Frame)
- 24** The universe and the reality of its creator  
» John G. Hartnett  
» *The Singular Universe and the Reality of Time: A Proposal in Natural Philosophy* (Roberto Mangabeira Unger, Lee Smolin)  
» *Time Reborn: From the Crisis in Physics to the Future of the Universe* (Lee Smolin)
- 26** A distorted map  
» Andrew Kulikovsky  
» *Mapping the Origins Debate: Six Models of the Beginning of Everything* (Gerald Rau)
- 30** Death-camp doctors—Darwin's proctors  
» Jerry Bergman  
» *Giants: The Dwarfs of Auschwitz* (Eilat Negev and Yehuda Koren)
- 34** Another devastating critique of neo-Darwinism  
» Dominic Statham  
» *Evolution: Still a Theory in Crisis* (Michael Denton)
- 38** A look into *The Unseen Realm*  
» Lita Cosner  
» *The Unseen Realm: Recovering the supernatural worldview of the Bible* (Michael S. Heiser)
- 40** Atheist fantasies vs fact  
» John Woodmorappe  
» *Faith vs Fact: Why Science and Religion are Incompatible* (Jerry A. Coyne)

## LETTERS

- 46** Catastrophic plate tectonics and plate tectonics—a comparison of two theories  
» Timothy L. Clarey  
» REPLY: Mark McGuire
- 48** Creationism in Europe  
» Philip Bell  
» REPLY: Jerry Bergman
- 50** Cnidarians turn evolutionary theory into jelly  
» Brian Thomas  
» REPLY: Jean O'Micks
- 51** Examining the floating forest hypothesis: a geological perspective  
» John D. Matthews  
» REPLY: Timothy L. Clarey





*The emergence of pathogenic bacteria impacts on concepts of God's character*



*In trying to explain complex phenomena, some evolutionists suggest that stones possess protomental properties.*

## VIEWPOINT

- 54** The Ice Age as a mechanism for post-Flood dispersal  
» Timothy L. Clarey

## PAPERS

- 60** Promoter evolution is impossible by random mutations  
» Jean O'Micks
- 67** Flood processes into the late Cenozoic—sedimentary rock evidence  
» Michael J. Oard
- 76** Origins of pathogenic microbes: part 1—bacteria  
» Warren A. Shipton
- 83** The overthrusting paradox: a challenge to uniformitarian geology and evolution  
» John D. Matthews
- 92** DNA topoisomerases—the 'relaxers' and 'unknotters' of the genome  
» Joe Deweese
- 102** The genetic effects of the population bottleneck associated with the Genesis Flood  
» Robert W. Carter and Matthew Powell
- 112** Young evidences in an ancient landscape: part 2—high-altitude sapping  
» Kenneth H. Karle

## ESSAYS

- 122.** Thinking correctly about science  
» Martin Tampier

## ABOUT US



### What is Creation Ministries International Ltd?

*Creation Ministries International Ltd.* is an independent, non-profit, non-denominational organization, controlled by Christians in the fields of science and education, committed to researching, developing, and promoting Christian creationist materials, and Christian school texts and aids. Our work is based on acceptance of:

- » The Bible is the written Word of God. It is divinely inspired and inerrant throughout.
- » The final guide to the interpretation of Scripture is Scripture itself.
- » The account of origins presented in Genesis is a simple but factual presentation of actual

events and therefore provides a reliable framework for scientific research into the question of the origin and history of life, mankind, the earth and the universe.

- » Scripture teaches a recent origin for man and the whole creation.
- » The great Flood of Genesis was an actual historic event, worldwide (global) in its extent and effect.
- » The special creation of Adam (as one man) and Eve (as one woman) and their subsequent fall into sin, is the basis for the necessity of salvation for mankind (and thus for the Gospel of Jesus Christ).
- » The scientific aspects of creation are important, but are secondary in importance to the proclamation of the Gospel of Jesus Christ as Sovereign, Creator, Redeemer and Judge.

Please note that in all of this, we openly proclaim

that our work is centred around Jesus Christ. We are convinced that the real needs of men and women can only be met by reconciliation to God through faith in and commitment to Jesus Christ the Creator, as Lord and Saviour.

© *Creation Ministries International Ltd.* All rights reserved. No part of this journal may be reproduced in any manner without written permission.

AN EXCEPTION is made where for study or for review purposes permission is granted for limited amounts of this publication to be copied provided due acknowledgment is given.

The views expressed in *Journal of Creation* are those of the writer(s) and not necessarily those of the Editors of *Journal of Creation* or the Directors of *Creation Ministries International*.

For instructions to authors, see the last page.



# How may the presence of mantle water be interpreted?

Michael J. Oard

Mantle and crustal rocks may contain water as part of their mineral phase. It is estimated that these rocks contain between 0.5 and 5 times the volume of the current oceans.<sup>1</sup> Olivine in the upper mantle has extremely little water, as interpreted from electrical conductivity measurements.<sup>1</sup> However, laboratory measurements show mantle transition zone minerals can potentially contain 2–2.5% water.<sup>2,3</sup> In the transition zone, located 410–660 km below the earth's surface, the increased pressure causes more compressed and denser phases of olivine and other upper mantle minerals to form. Wadsleyite generally occurs above 510 km depth, ringwoodite is generally found at 510–660 km depth, and majorite-garnet occurs throughout the whole transition zone (figure 1).<sup>4</sup> The deep mantle below 660 km is expected to be *anhydrous* high-pressure phases of mostly olivine.<sup>2</sup>

## An amazing mantle sample of ringwoodite

Recently, the first sample of ringwoodite was found in a mineral inclusion within a diamond. This confirms estimates of the amount of water in the transition zone.<sup>2,3</sup> Diamonds usually originate below 140 km but some are believed to have originated from the transition zone or below.<sup>5</sup> Ringwoodite and wadsleyite should have reverted to olivine in kimberlites, small intrusions that contain diamonds.<sup>4</sup> However, the uplift of the rock in the kimberlite must

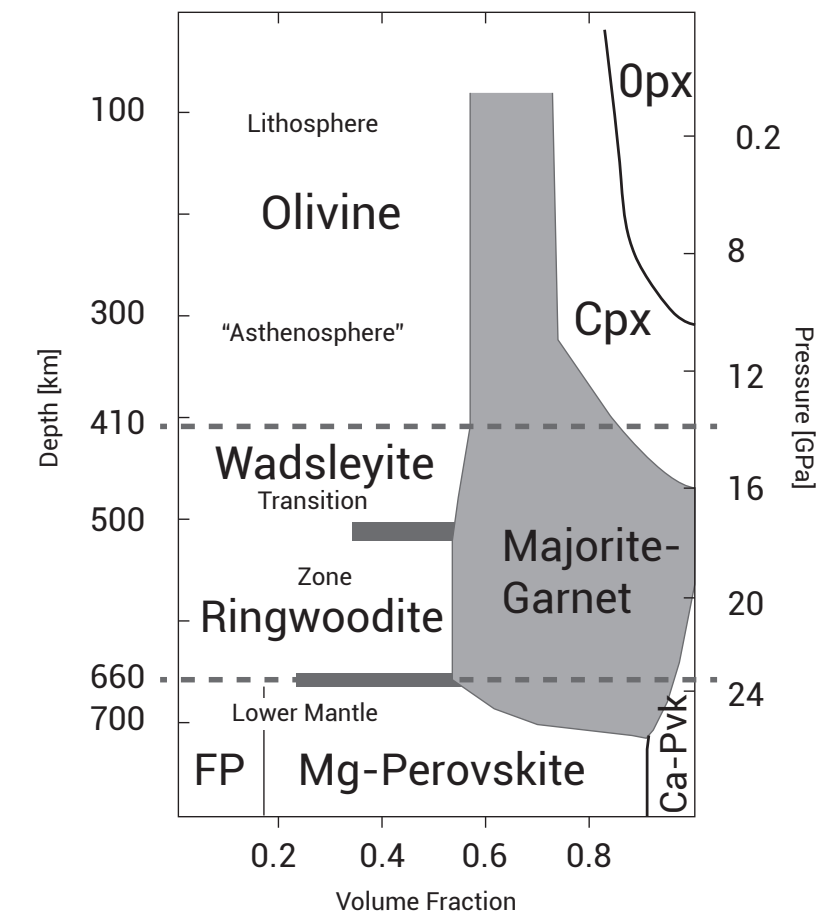


Figure 1. Relative mineral proportions and phase transitions in the earth's mantle<sup>4</sup>

have been extremely rapid, so that the transition zone minerals did not change.<sup>3</sup> The ringwoodite inclusion contained a minimum of 1.5% water.

## How much water in the transition zone?

How representative of the amount of water in the transition zone is this one sample? Pearson *et al.* conservatively estimate that, at least locally, the transition zone has about 1% water. This is also consistent with measured seismic wave velocities<sup>2</sup> and with the water content of some kimberlites.<sup>3</sup> If the amount of water in the ringwoodite is representative for the lower part of the transition zone (510–660 km depth), then a speculative estimate suggests that this layer contains about  $1.4 \times 10^{21}$

kg of water; about the same mass as found in the present oceans.<sup>3</sup> This does not include the water in wadsleyite in the upper transition zone, which is suggestive of an equivalent amount.

## What could high water content in the transitional zone mean?

Secular scientists presume that over billions of years, the oceans collected their water from volatile outgassing from the mantle. Now they have a possible source for the oceans in their deep-time model.

How should creationists interpret the possibility of large quantities of water in the mantle transition zone? Could the water for the Flood have originated from the mantle, as a few creationists have suggested? It is doubtful, since there are about 400 km

of dry olivine and other upper mantle minerals between the surface and the transition zone. Moreover, how would this water be released from the minerals? If it could be released, a huge amount of ringwoodite and wadsleyite in the form of olivine and other mantle minerals would have uplifted to the earth's surface in some giant overturning. On the contrary, there is very little exposed mantle rock at the earth's surface.

Could runaway subduction in the Catastrophic Plate Tectonics (CPT) model transport water down to where it can be absorbed within transitional zone minerals? This is possible but only on a local or regional scale. Maybe if the water in the transitional zone is rare, CPT could explain it. But, then there is the problem of how water from a subduction zone can end up within the mineral lattice of ringwoodite and wadsleyite.

Given this information and considering the uncertainties in the estimated quantities, a third option seems most likely: the water was placed in the transition zone at Creation. The alternatives seem too improbable in comparison.

## References

1. Knan, A. and Shankland, T.J., A geophysical perspective on mantle water content and melting: inverting electromagnetic sounding data using laboratory-based electrical conductivity profiles, *Earth and Planetary Science Letters* **317**–**318**:27–43, 2012.
2. Pearson, D.G., Brenker, F.E., Nestola, F. *et al.*, Hydrous mantle transition zone indicated by ringwoodite included with diamond, *Nature* **507**: 221–224, 2014.
3. Keppler, H., Earth's deep water reservoir, *Nature* **507**:174–175, 2014.
4. Stachel, T., Brey, G.P. and Harris, J.W., Inclusions in sublithospheric diamonds: glimpses of deep Earth, *Elements* **1**:73–78, 2005.
5. Harte, B., Diamond formation in the deep mantle: the record of mineral inclusions and their distribution in relation to mantle dehydration zones, *Mineralogical Magazine* **74**(2):189–215, 2010.

# The fruit of sin vs the fruit of sanctification: a Pauline allusion to Genesis 3 in Romans 6

Lita Cosner

Paul's allusions to Genesis in the book of Romans have been widely acknowledged, especially in Romans 1:20ff;<sup>1</sup> 5:12–21;<sup>2</sup> and 8:19–23.<sup>3</sup> I propose there is an additional, commonly overlooked, allusion to Genesis 3 in Romans 6:20–23, which is clear when we look at the constellation of terms Paul uses:

“For when you were slaves of sin, you were free in regard to righteousness. But what fruit were you getting at that time from the things of which you are now ashamed? For the end of those things is death. But now you have been set free from sin and have become slaves of God, the fruit you get leads to sanctification and its end, eternal life. For the wages of sin is death, but the free gift of God is eternal life in Christ.”

In Romans 5, Paul depicted Adam and Christ as two heads of humanity, whose respective rebellion and obedience resulted in death and life, respectively, for those under them. Here Paul depicts two modes of life, one unbelieving and one believing, which bear different fruits with different consequences. The first is slavery to sin and freedom from righteousness, which bears shameful fruit which leads to death. This was the life every one of the Roman believers in Paul's original audience lived before believing in Christ. The second is their current life, slavery to God and freedom from

bondage to sin, which bears the fruit of sanctification which leads to eternal life.

## Fruit leading to shame and death; fruit leading to eternal life

One can make a lexical argument that Paul is continuing to reference the Fall narrative (Genesis 3) in this passage. There are several words which occur both in the Fall narrative and in this passage. The word καρπός (*karpos*, fruit) occurs both in Genesis 3:2–3, 6 LXX and in Romans 6:21–22. The word translated ‘ashamed’ occurs in Genesis 2:25 LXX (αἰσχύνομαι, *aischunomai*) and Romans 6:21 (ἐπαισχύνομαι, *epaischunomai*). The verb translated ‘to die’ (ἀποθνήσκω, *apothnēskō*) occurs in Genesis 3:3–4 LXX, and the related noun translated ‘death’ (θάνατος, *thanatos*) occurs in Romans 6:21 and 23. The fact that in both Genesis 3 and Romans 6, fruit leads to shame and death is more significant than the mere presence of the same constellation of terms.

In both Genesis 2–3 and Romans 6, fruit also leads to eternal life. In Genesis 2–3, this is the fruit of the tree of life, from which Adam and Eve were free to eat prior to the Fall. However, after the Fall, they were removed from the Tree of Life to *prevent* their eating and living forever. But as Paul says: “But now that you have been set free from sin and have become slaves of God, the fruit you get leads to sanctification and its end, eternal life” (Romans 6:22). This is consistent with the image of believers having free access to the Tree of Life in the New Jerusalem (Revelation 22:2).

## Interpretive and translational issues

Incidentally, recognizing this reference may help to resolve an interpretive debate about this passage.



ὅτε γὰρ δοῦλοι ἦτε τῆς ἀμαρτίας, ἐλεύθεροι ἦτε τῇ δικαιοσύνῃ. τίνα οὖν καρπὸν εἶχετε τότε; ἐφ' οἷς νῦν ἐπαισχύνεσθε, τό γὰρ τέλος ἐκεῖνων θάνατος. νυνὶ δὲ ἐλευθέντες ἀπὸ τῆς ἀμαρτίας δουλωθέντες δὲ τῷ θεῷ ἔχετε τὸν καρπὸν ὑμῶν εἰς ἀγιασμόν, τὸ δὲ τέλος ζωὴν αἰώνιον. τὰ γὰρ ὀψώνια τῆς ἀμαρτίας θάνατος, τὸ δὲ χάρισμα τοῦ θεοῦ ζωὴ αἰώνιος ἐν Χριστῷ Ἰησοῦ τῷ κυρίῳ ἡμῶν.

Figure 1. The Greek text of Romans 6:20–23 as punctuated by UBS5

There are two ways to punctuate Romans 6:21. The first is that preferred by the ESV: “But what fruit were you getting from the things of which you are now ashamed? For the end of those things is death.” In this punctuation, the assumed answer to the rhetorical question is ‘none’, because ‘fruit’ in this instance is assumed to mean ‘good results’. As Murray explains:

“In paraphrase the thought would be as follows: ‘Present your members servants to righteousness unto holiness (vs. 19). For consider that in your former state of service to sin you had no concern at all for righteousness and no good fruit whatsoever accrued from abandonment to the service of sin, nothing indeed but that of which you are now ashamed and the end of which is death. How urgent, therefore, is the claim of righteousness and the necessity of commitment to its bondservice.’”<sup>4</sup>

The second option is: “Therefore, what fruit did you have then? That of which you are now ashamed. For the end of these is death.”<sup>5</sup> Because καρπός normally has a positive connotation in Paul’s writing, most commentators prefer the first option. However, some disagree.

“‘Fruit’ is mostly used by Paul in a good sense and some argue for a good sense here, but F. Hauck is probably right when he comments, ‘The pre-Christian man is under the power of sin and brings forth the

corresponding fruits’ (TDNT, II, p. 615). Paul is inquiring what really significant result had followed from their living in those evil ways of which they are now ashamed. The end of those things, he emphasizes is death.”<sup>6</sup>

This interpretation also makes the most sense of the proposed Genesis 3 reference. In any case, a negative connotation to καρπός is not foreign to the usage of the rest of the New Testament, see for instance Matthew 7:16–20.

Also, this passage highlights the consequences of taking a ‘dynamic equivalence’ translation too far, because it may obscure parallels the author intends to bring to mind. For instance, the NIV translates *karpos* as ‘benefit’, erasing the idea of ‘fruit’ from the passage and making it much harder to see any parallel to Genesis. As Morris points out: “Interestingly, NIV removes the agricultural metaphor by translating *benefit* where the noun means ‘fruit’ and then inserts it by rendering *reap* where the verb means ‘have’.”<sup>6</sup> Other dynamic equivalence translations similarly obscure the original terminology, making it harder to see that there are two interpretive options with the sentence in verse 21, as well as a parallel to Genesis 3. Only the strict translation of ‘fruit’ preserves the ambiguity inherent in the original Greek.

## What is ‘the sin’?

Paul concludes this passage: “For the wages of sin (τῆς ἀμαρτίας, *tēshamartias*) is death, but the free gift of God is eternal life in Christ Jesus our Lord.” The singular noun is significant:

“Paul does not say ‘The wages of *our sins* is death’ but, ‘The wages of *the sin* is death’. Since 5:12 we have seen that this articulated term ‘the sin’ denotes, not sin and sinning in general (which is ἀμαρτία without the article), but ‘the power of sin’. It is a kind of personification. Like a master ‘the sin’ pay [sic] wages, namely this sin power that entered the world by the one act of Adam and by that one act enslaved us all. Nor should we forget that ‘the death’ came in with ‘the sin’ and by its very coming got hold of us all.”<sup>7</sup>

This reveals that Paul does not leave the comparison he was making beginning in Romans 5:12–21; rather, he is carrying it through to the end of chapter 6. This helps us to understand the flow of Paul’s thought, and reveals more about how he thinks of Adam’s *historical* sin as having actual consequences in the lives of the believers to whom he is writing.

## References

1. Kulikovskiy, A.S., Scripture and general revelation, *J. Creation* 19(2):23–28, 2005; creation.com/genrev.
2. Cosner, L., Romans 5:12–21: Paul’s view of a literal Adam, *J. Creation* 22(2):105–107, 2008; creation.com/romans5.
3. Smith, H.B., Jr, Cosmic and universal death from Adam’s fall: an exegesis of Romans 8:19–23a, *J. Creation* 21(1):75–85, 2007; creation.com/romans8.
4. Murray, J., *The Epistle to the Romans*, Eerdmans, Grand Rapids, MI, p. 235, 1960.
5. Moo, D.J., *The Epistle to the Romans*, New International Commentary on the New Testament, Eerdmans, Grand Rapids, MI, p. 406, 1996.
6. Morris, L., *The Epistle to the Romans*, Pillar New Testament Commentary, Eerdmans, Grand Rapids, MI, p. 266, 1988.
7. Lenski, R.C.H., *The Interpretation to St. Paul’s Epistle to the Romans*, Lutheran Book Concern, Columbus, OH, p. 435, 1936.

# Samotherium fossils and variation in the neck within the giraffe kind (Giraffidae)

Jean K. Lightner

Popular level summaries of scientific research often use catchy headlines and phrases to capture the reader's attention, even if they are a bit misleading. Recently a summary claimed: "Fossil bones from extinct cousin reveal how giraffe got its long neck" and that "It has long been thought that the giraffe's neck was a result of evolution, but fossil evidence had been lacking."<sup>1</sup> The fossils don't really tell us how the giraffe got its long neck, but the scientific study referred to does provide important information on how cervical vertebrae vary within the family Giraffidae. Since the giraffe, okapi, and bones from extinct members of this family are considered by creationists to belong to creatures from a single created kind, the types of differences identified are welcome information to help us understand how God designed creatures of this kind to vary.<sup>2</sup>

Skeletal variation is common in mammals, even within a single species. In domestic pigs the number of thoracic and lumbar vertebrae can vary, and the underlying genetic basis of this variation is being uncovered.<sup>3</sup> Yet it is far more common for the size and shape of vertebrae to vary. For example, variation in the vertebral processes of the cervical spine in horses has been described. In one case the variation was correlated to breed; in another it was correlated with the sex of the horse.<sup>4</sup> Also, some sheep

(e.g. the Nubian breed) have large (interarcual) spaces between several cervical vertebrae.<sup>5</sup>

## The long-necked giraffe

Despite its incredibly long neck, the giraffe has the same number of cervical vertebrae (seven) as nearly all other mammals.<sup>6</sup> The increase in length is primarily due to an increased rate of growth in that dimension of all its cervical vertebrae, most of which takes place after birth.<sup>7</sup> These neck bones make up half the total length of the spinal column by the time the giraffe is full grown. There is some restructuring that appears in various regions of the spinal column too. The first thoracic vertebra bears similarities to the last cervical vertebra in other species. Additionally, the transverse processes are enlarged to support the modified muscles that support the neck.<sup>8</sup>

The only two species of the giraffe family that are alive today, the giraffe and the okapi, are on opposite ends of the spectrum when it comes to neck length. Based on fossil evidence it is suggested that the giraffe had an ancestor with a much shorter neck.<sup>9</sup> The study highlighted by the popular level news release involved detailed study of fossil cervical vertebrae from *Samotherium major*, 'an intermediate-necked giraffid', and comparison of the measurements to those from the giraffe and okapi.<sup>10</sup>

## Holding the head up high

The authors address the position the neck is held at in the resting animal as it relates to the shape of the vertebrae and features of the skull. In some ruminants the head is held relatively horizontal, with the first cervical vertebrae (atlas, or C1) nearly the same level as the last (C7). This is seen in animals such as cattle and African buffalo. A semi-vertical position,

where the cervical vertebrae are held around a 45° incline, is seen in the okapi and various species of gazelle. A more vertical position, with a greater than 60° incline in the resting animal, is seen in the gerenuk (a long-necked species of antelope) and the giraffe. Skeletal features of *S. major* seem to be most similar to the latter based on certain features of C1, C7 and the position of the palatine indentation (figure 1). Thus they conclude that *S. major* held its neck in a vertical position.

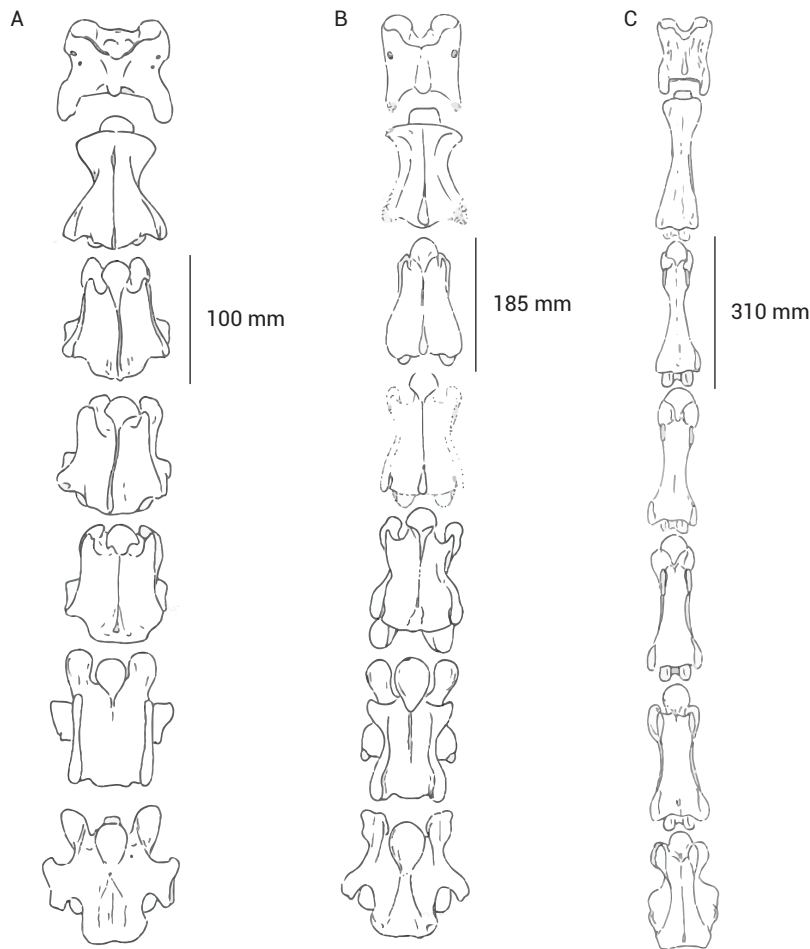
There are other anatomical findings in *S. major* that are uncharacteristic of ruminants, namely a wedge shape of the cervical vertebrae as viewed from the side. Several muscles from the thorax insert in the caudal region of the cervical vertebrae, and the authors believe these regions are thicker in *S. major* to allow for a broader attachment. They feel this further supports their inference of a vertical position of the neck. *S. major* has other features not seen in either the giraffe or okapi. For example there are differences in the position of spinous process on C2 that may have allowed for more dorsal flexion of the head.

## Samotherium, fitting in between

In the upper region of the spine (C2–C3; see figure 1) *S. major* has features that were a mosaic of okapi and giraffe characteristics. For example, the angle of the dorsal tubercle was similar to the okapi, while the angle of the spinous process was more similar to the giraffe. This pattern was seen for a number of other measurements in this region. In contrast, the more caudal cervical vertebrae (C5–C7) tended to be intermediate between the extant species.

The authors discuss a previous study where it was found that the cranial region of vertebrae were lengthened in fossils believed to be





**Figure 1.** C1–C7 vertebrae (from top to bottom) of (a) *Okapia johnstoni*, (b) *Samotherium major*, and (c) *Giraffa camelopardalis* (figure 7 from Danowitz, Domalski, and Solounias<sup>10</sup>).

from giraffids with an intermediate neck length. The giraffe has lengthening in both the cranial and caudal aspects of its vertebrae. So in this characteristic, *S. major* is believed to have undergone the first of two steps in neck lengthening, lengthening of the cranial portion of the cervical vertebrae.

While *S. major* is not considered a direct ancestor of the giraffe, it is exceptional in that an almost complete neck has been found. From the comparisons that have been made we can see that changes in neck length are complex and not just a matter of scaling. The extra length has implications for muscle attachments to adjust for the stress (extra weight with an increased moment arm) and

changes in head carriage. Other body systems must adjust as well.<sup>11</sup>

### Conclusion

Evolution is often defined as change over time. Thus, evolutionists often point to changes within created kinds and claim it is evidence for evolution, the idea that all animals share common ancestry. In the case of the giraffe family, there certainly have been changes. However, they do not support universal common ancestry. Within kind changes require that there is design to allow for the body to change without destroying the animal. Changes in size, shape, and even number of vertebrae require both an animal designed with these

skeletal features as well as design in the animal to allow for changes (e.g. so the muscles still attach well and are useful). It is consistent with an awesome Designer who created his creatures to reproduce and fill the earth (Genesis 1:22; 8:15–17; Isaiah 45:18), adapting to various environments as they did so.

### References

- Cooper, D., Fossil bones from extinct cousin reveal how giraffe got its long neck, [www.abc.net.au/news/2015-11-25/fossil-bones-from-extinct-cousin-reveal-how-giraffe-got-its-neck/6970488](http://www.abc.net.au/news/2015-11-25/fossil-bones-from-extinct-cousin-reveal-how-giraffe-got-its-neck/6970488), accessed 6 January 2016.
- It is not completely clear if the level of the kind is at the family, Giraffidae, or higher at the suborder, Ruminantia. Lightner, J.K., Mammalian Ark kinds, *Answers Research J.* 5:151–204, 2012; pp. 151, 191–193.
- Rohrer, G.A., Nonneman, D.J., Wiedmann, R.T. and Schneider, J.F., A study of vertebra number in pigs confirms the association of vertnin and reveals additional QTL, *BMC Genetics* 16:129, 2015.
- Santinelli, I., Beccati, F., Arcelli, R. and Pepe M., Anatomical variation of the spinous and transverse processes in the caudal cervical and the first thoracic vertebrae in horses, *Equine Veterinary J.* 48(1):45–49, 2016.
- Turkof, E., Jurasch, N., Grassberger, M., Schwendenwein, S., Habib, D., Knolle, E. and Losert, U., Large interarcuate spaces in the cervical vertebral column of the Tyrolean mountain sheep, *Anatomia, Histologia, Embryologia* 32(1):9–11, 2003.
- Badlangana, N.L., Adams, J.W. and Manger, P.R., The giraffe (*Giraffa camelopardalis*) cervical vertebral column: a heuristic example in understanding evolutionary processes? *Zoological J. Linnean Society* 155(3):736–757, 2009. The only known mammals to vary from the usual seven cervical vertebrae are manatees (*Trichechus*) and sloths (*Bradypus* and *Choloepus*). This is in contrast to other vertebrate orders (e.g. birds, amphibians) where variation in the number of cervical vertebrae is quite common.
- van Sittert, S.J., Skinner, J.D. and Mitchell, G., From fetus to adult—an allometric analysis of the giraffe vertebral column, *J. Experimental Zoology Part B: Molecular and Developmental Evolution* 314(6):469–479, 2010.
- Endo, H., Yamagiwa, D., Fujisawa, M., Kimura, J., Kurohmaru, M. and Hayashi, Y., Modified neck muscular system of the giraffe (*Giraffa camelopardus*), *Annals of Anatomy* 179(5):481–485, 1997.
- Badlangana, et al., ref. 6.
- Danowitz, M., Domalski, R. and Solounias, N., The cervical anatomy of *Samotherium*, an intermediate-necked giraffid, *Royal Society Open Science* 2(11):150521, 2015.
- Paton, J.F.R., Dickinson, C.J. and Mitchell, G., Harvey Cushing and the regulation of blood pressure in giraffe, rat and man: introducing ‘Cushing’s mechanism’, *Experimental Physiology* 94(1):11–17, 2009.

# Pluto's moons a big surprise!

John G. Hartnett

Most inner moons in the solar system keep one face pointed towards their central planet. This is claimed to have resulted from a gravitational tidal locking effect that is evidence for the very old age of the solar system (allegedly about 5 Ga). Due to the fact that the moons are not point objects, gravitational theory tells us ‘tidal friction’ causes the moons to eventually tidally lock to their respective planets after a long period of time, thus leaving one face of the moon always pointed at the parent planet. Therefore the moons rotate on their axis once per revolution around their parent planet.

## Spinning tops around Pluto

But the animation referenced below,<sup>1</sup> which has come from NASA's recent analysis of Pluto, shows that this certainly isn't the case with the small moons of Pluto. They behave like spinning tops. In the illustration below, Pluto is shown at centre with its moons Charon, Styx, Nix, Kerberos, and Hydra. New analysis has found that the 4 smaller moons—Styx, Nix, Kerberos, and Hydra—rotate surprisingly rapidly as they orbit Pluto (now known as a dwarf planet) with its companion moon Charon.

The small moons—Styx, Nix, Kerberos, and Hydra, in order of proximity to Pluto—all rotate much faster than the 20 to 38 days the moons take to orbit the Pluto-Charon system. Kerberos spins the slowest, once every 5.33 hours, whereas Hydra is the whirling dervish of the quartet, rotating once every 26 minutes.<sup>2</sup>

“These Pluto moons are essentially spinning tops, and

that radically changes the way we understand the dynamics of how they operate’, planetary scientist Mark Showalter of NASA's New Horizons mission and of the SETI Institute in Mountain View, Calif., told *Eos* ... ‘This is unlike anything we’ve seen elsewhere in the solar system’, he added. ‘No one has ever seen a moon (like Hydra) that rotates 89 times during a single orbit.’”<sup>2</sup>

Prior to the New Horizons mission it was believed, from Hubble Space Telescope images, that the moons’ orbits were chaotic. But from the data recorded by the Long Range Reconnaissance Imager camera on the New Horizons spacecraft during its fly-by of this system, it has been determined that the brightness variations from the moons show very clear signs of periodicity, revealing that the moons were not so much tumbling but spinning in a regular fashion, and much faster than anyone expected. The images also reveal that Nix is orbiting backward and on its side.<sup>1</sup> In addition, from the animation above, you may note that the spin axes of the moons are precessing, just like a spinning top. (Towards the end of the video one moon is illustrated with its spin axis precessing or rotating.) This usually indicates a recent disturbance. Could it mean a recent creation?

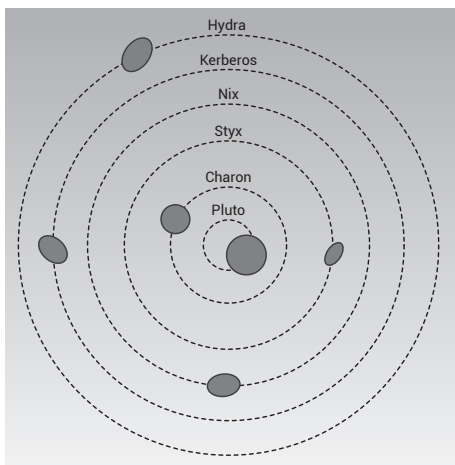


Figure 1. Pluto/Charon and their moons (NASA/JHUAPL/SwRI/Mark Showalter)

## Challenge to uniformitarian theory

And where does that leave the uniformitarian theory for the formation of the solar system? In big trouble, I suggest. Some *ad hoc* hypothesis must now be invented to explain this anomaly. Perhaps, they'll say, Kuiper Belt objects continually are disturbing the moons and thus have not allowed them to settle into tidally locked positions over the alleged billions of years since they formed. Or that these are planetoids captured by the dwarf planet Pluto more recently and hence have not had time to lock up. But it will be more storytelling, for sure. Just wait for it!

And Nix rotates retrograde—backwards—similar to the way the planet Venus orbits the sun. Nix is also on its side similar to the planet Uranus (which has a 97.77% tilt to the plane of the solar system). These are anomalies that are contrary to the uniformitarian principle of the solar system forming out of a nebula cloud of gas and dust.<sup>3,4</sup> In such a scenario all angular momentum is directed in the same plane. The angular momentum vector should be perpendicular to the plane of the alleged newly forming protoplanetary system. How can individual planets and moons spin retrograde? That would mean their angular momentum vector points in the opposite direction to the rest of the bodies. Also, of course there should really be little angular momentum in the outer planets as the sun allegedly spun up. But the opposite is needed, because the sun is observed to have relatively very little angular momentum.

Consider our sun with a mass representing 99.86% of the mass of the solar system but only 4% of its angular momentum. The planets on the other hand have a total combined mass of only 0.14% of the mass of the solar system yet 96% of its angular momentum. Most of the angular momentum of any solar system must reside initially



in the central core of the collapsing cloud, which eventually becomes the star, *according to the theory*. Yet, after some time nearly all the angular momentum has to be transferred to the planets somehow. *This is a huge problem for the theory.*<sup>2,5,6</sup>

Earth's moon was created in a near perfect circular orbit and tidally locked for purposes of stability to Earth's tides and other designed-for-life features. Any disturbance to the orbit or any notion that it could have been captured run counter to its observed near perfectly circular orbit. Likewise, planets with tidally locked moons were created that way, as well as retrograde motion like Venus' spin. Naturalistic methods fail on all counts to account for such a feature.

In the case of Pluto, the moons may be captured smaller Kuiper Belt objects. Pluto itself may be such, since it has a highly eccentric orbit, even out of the plane of the rest of the planets. And the high spin rates of its moons testify at least that such an event did not occur billions of years ago, else they would be tidally locked today.

A created solar system, which is only 6,000 years old, is consistent with these observations. It is also consistent with tidally locked moons and anomalous rotation directions of some of the solar system bodies. Creation is a far simpler explanation for the formation of this system.

## References

1. Pluto's Spinning Moons, youtube/ei5aF6Bw56E NASA.gov video, Credit: NASA/JHUAPL/SwRI/Mark Showalter.
2. Cowen, R., New spin on Pluto's moons, Eos, 96, eos.org/articles/new-spin-on-plutos-moons, doi:10.1029/2015EO039209, 9 November 2015.
3. Hartnett, J.G., A 'protoplanetary system' information? bible-scienceforum.com/2015/09/28/a-protoplanetary-system-in-information/, 28 September 2015.
4. Hartnett, J.G., Development of an 'old' universe in science, bible-scienceforum.com/2015/07/30/development-of-an-old-universe-in-science/, see section 'Nebular hypothesis', 30 July 2015.
5. Hartnett, J.G., Giant molecular clouds, creation.com.
6. Hartnett, J.G., Planetary system formation: exposing naturalistic storytelling, creation.com.

# The uniformitarian puzzle of mountaintop planation surfaces

Michael J. Oard

Planation surfaces are a common feature across the earth.<sup>1,2</sup> But secular researchers often find these surfaces perplexing because it is not unusual to find them at the top of rugged mountains (figure 1):

"Extensive tracts of low-gradient topography in steep mountain ranges, either forming rangetop plateaus or terraced pediments on range flanks are widely distributed in mountain belts around the world."<sup>3</sup>

Calvet *et al.*'s survey of these flat-topped mountains establishes their frequency across the globe.<sup>4</sup> Calvet *et al.* also point out that they are even found atop some of the most active

and rapidly eroding mountains on the planet.

## Uniformitarian scientists cannot explain

What makes these planation surfaces so puzzling for uniformitarian scientists is that they are not currently forming and their past formation appears to be independent of variables, such as rock lithology and the tilt of sedimentary rocks.<sup>5</sup> The authors admit they *cannot* explain these mountaintop planation surfaces:

"Such low-gradient features are enigmatic given that an expected >50% of total denudation and 40% of chemical denudation occur on the steepest ~10% of the Earth's continental surface, i.e., mainly in mountains . . . This would suggest that the chances of survival of planar landforms in mountain environments are slim."<sup>6</sup>

## Some ideas rejected arbitrarily

It is interesting that although the secular scientists cannot explain planation or erosion surfaces, they are not open to the possibility that this could be a signature of a global



**Figure 1.** Gypsum Mountain, north-west Wind River Mountains, Wyoming, USA. The strata dip to the west at about 40°, but they have been planed flat.

flood. They reject my explanation simply because I am a creationist: “(note; here we ignore creationist views of planation surfaces, e.g. michael.oards.net/).”<sup>6</sup> They also reject the explanation provided by Ollier and Pain, apparently because Ollier and Pain do not fully accept plate tectonics.<sup>7</sup> Ollier and Pain believe strata were first folded, then planed in the Miocene, the early part of the late Cenozoic, and then were uplifted globally during the Pliocene and Pleistocene, the very late Cenozoic.<sup>8</sup> Accordingly most of the planing was done before mountain formation.

### Planation surfaces and pediments carved by Flood runoff

Ollier and Pain’s explanation of the event sequence for the formation of mountaintop planation surfaces is generally correct, but they are unable to keep planation surfaces from eroding over millions of years, making it likely that their understanding of the timeframe is wrong. Calvet *et al.*’s argument is weaker than that of Ollier and Pain, because with no clear way to connect planation surfaces in their framework to a single event, or even a single suite of causes, they are forced to resort to unknown ‘case-by-case conditions’ to explain the phenomena they observe.<sup>9</sup> They truly have no idea how to explain mountaintop planation surfaces.

The fundamental problem for both Ollier and Pain and Calvet *et al.* is deep time. Eons of time attenuates the link between causes and effects so much that it’s practically impossible to establish causal links between observed effects. The Flood, however, is a specified event in which the duration is sufficiently short to enable the investigator to posit plausible causal links in observed geological phenomena and their relationships, and an adequate cause for the

phenomena we see. In other words, a plausible cause-effect narrative has a better chance of being constructed in the context of Noah’s Flood.<sup>10</sup>

In the case of mountaintop planation surfaces, they are best explained as a function of the Recessive Stage of the Flood. During Flood water runoff, the continents and mountains rose with much erosion.<sup>1,2,11</sup> It is expected that during uplift rapid currents would plane the top of the rocks by erosion. Continued uplift and channel erosion would divide large planation surfaces into isolated remnants near the tops of the mountains. At lower elevations this erosion would divide the planation surfaces into large areas, such as plains or plateaus, depending upon the amount of uplift. The major planing episodes would have happened during the Abative or Sheet Flow Phase of the Flood.<sup>12</sup>

As mountains and plateaus rose above the Flood water, the water was forced to channelize down valleys. Within mountain valleys, fast flow toward the sinking ocean basins created planation surfaces along the edge of the mountains, called pediments.<sup>1,2,13</sup> The planation surfaces and pediments still exist because there was insufficient time for erosion to destroy these features, especially in arid to semi-arid areas. The lack of erosion provides another piece of evidence that deep time is an invalid construct, and that planation surfaces are very young.

Ollier and Pain would date the mountaintop planation surfaces as mid Cenozoic. Calvet and colleagues would also date them as mostly Cenozoic: “The presence of erosion surfaces in many mountain ranges of *Cenozoic* age raises issues [emphasis added]”.<sup>14</sup> Given this designation, in the biblical framework the great mountain uplifts and planing occurred in the last half of the Flood during Flood runoff<sup>15</sup> or in the Recessive Stage.<sup>10</sup> This would indicate a largely late Cenozoic Flood/

post-Flood boundary in areas with planation surfaces and pediments, assuming the geological column for sake of discussion.

### References

1. Oard, M.J., *Flood by Design: Receding Water Shapes the Earth’s Surface*, Master Books, Green Forest, AR, 2008.
2. Oard, M.J., ebook, *Earth’s Surface Shaped by Genesis Flood Runoff*, 2013, Michael.oards.net/GenesisFloodRunoff.htm.
3. Calvet, M., Gunnell, Y. and Farinass, B., Flat-topped mountain ranges: their global distribution and value for understanding the evolution of mountain topography, *Geomorphology* **241**:255, 2015.
4. Calvet *et al.*, ref. 3, pp. 255–291.
5. Calvet *et al.*, ref. 3, pp. 279–281.
6. Calvet *et al.*, ref. 3, p. 256.
7. Ollier, C. and Pain, C., *The Origin of Mountains*, Routledge, London, 2000.
8. Oard, M.J., The Mountains Rose: Review of Cliff Ollier and Colin Pain, *The Origin of Mountains*, *J. Creation* **16**(3):40–43, 2002.
9. Calvet *et al.*, ref. 3, pp. 285.
10. A good example of this is documented by Reed, J.K., Changing paradigms in stratigraphy—a quite different way of analyzing the record, *J. Creation* **30**(1):83–88, 2016.
11. Oard, M.J., Surficial continental erosion places the Flood/post-Flood boundary in the late Cenozoic, *J. Creation* **27**(2):62–70, 2013.
12. Walker, T., A Biblical geological model; in: Walsh, R.E. (Ed.), *Proceedings of the Third International Conference on Creationism*, technical symposium sessions, Creation Science Fellowship, Pittsburgh, PA, pp. 581–592, 1994.
13. Oard, M.J., Pediments formed by the Flood: evidence for the Flood/post-Flood boundary in the late Cenozoic, *J. Creation* **18**(2):15–27, 2004.
14. Calvet *et al.*, ref. 3, p. 279.
15. Oard, M.J., *The Flood/Post-Flood Boundary Is in the Late Cenozoic with Little Post-Flood Catastrophism*, 2014, michael.oards.net/PostFloodBoundary.htm.



# The origin of meteorite chondrules

Michael J. Oard

Meteorites are claimed by secular scientists to be the rocky debris left over after the formation of the solar system. Chondrites, stone meteorites, represent 85% of the rocks that fall on the earth; the remaining 15% mostly are iron meteorites. Uniformitarian scientists believe the inner four rocky planets of the solar system, including the earth, were formed largely or totally of chondritic rock. That is one reason for the intense study of chondrites.

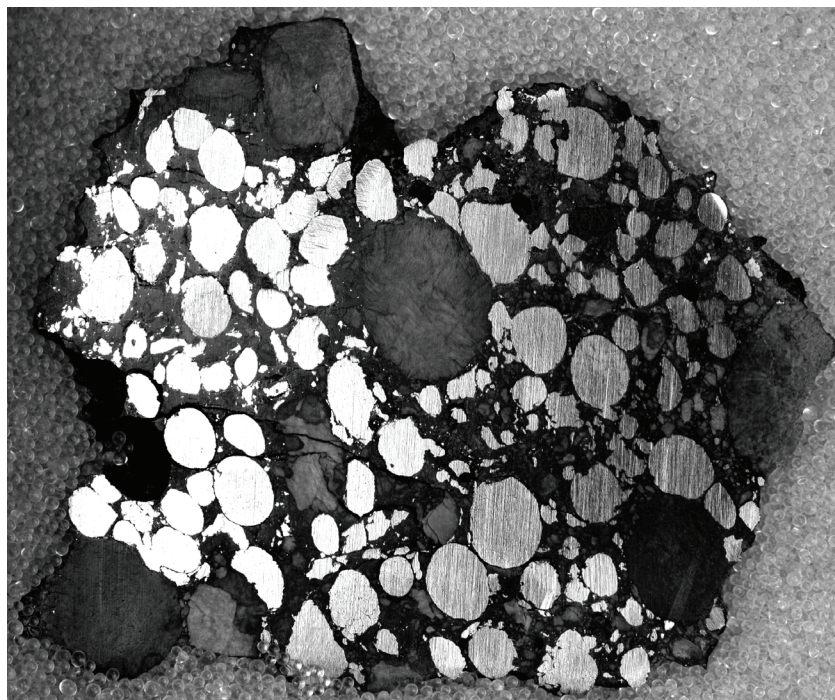
## Naturalistic origin of chondrites not even in sight

There are a number of problems with the secular understanding of the origin of chondrites. First, they cannot be observed forming today. Therefore, all ideas on the origin of chondrites go against the uniformitarian principle of ‘the present is the key to the past’. This is also true of all other ideas of origins in the solar system and universe.<sup>1,2</sup> Of course the researchers claim conditions were unique 4.5 billion years ago, so that solar system formation just happened to form.<sup>3</sup> But even with the special ‘back then’ conditions, there are other problems.

A second issue is the temperature necessary for meteorite and/or planet formation.

“But meteoriticists have been hard pressed to come up with enough energy even then to rapidly heat rocky dust to 1600 kelvin or more and melt it into globules. The nebula at the time was merely warm—at most several hundred kelvin.”<sup>1</sup>

Globules need to be melted in order to form chondrites. One



**Figure 1.** A 4.6 x 3.8 cm cross section of the Gujba meteorite found in Nigeria showing abundant chondrules (white spheres)

researcher was able to come up with 14 heating mechanisms for dust, which brings up a second problem, that such ideas cannot be tested:

“None [of the 14 heating mechanisms], Rubin noted, struck astrophysicists as particularly plausible. ... ‘There are a lot of models out there, but I’m not sure how you can really test them ...’”<sup>1</sup>

Evolutionary scientists have a number of hypotheses, but they need to consider whether their ideas make sense and whether they can be tested.

A third problem is the origin of chondrules within chondrites, the melted globules, which range in size from a few micrometres to a centimetre (figure 1). Chondrules are composed mostly of the silicate minerals olivine and pyroxene, thought to be common mantle rocks of the earth, embedded in a smooth matrix. Chondrules

“... form as molten or partially molten droplets in space before being accreted to their parent

asteroids. ... Chondrules are believed to have formed by a rapid (flash) heating (within minutes or less) and melting of solid dust aggregates of approximately Solar composition under temperatures of about 1000 K.”<sup>4</sup>

So, chondrules are believed to have been rapidly heated, anywhere from 1,000 to 1,600 K, and became molten before incorporation into its parent asteroid. Some chondrules have textures that show rapid cooling from a molten mass. Needless to say, such processes are beyond experimentation and testing.

An analysis of the chemistry, rock types, and isotopes reveals additional problems. Chondrules are quite diverse with four groups and 12 subgroups. There is no ‘normal’ type of chondrule, making it virtually impossible to come up with a uniform origin model. They have also retained their ‘volatiles’. Volatiles are those elements or minerals that are more easily vapourized. Why should chondrules

contain volatiles if they melt at hot temperatures? Moreover, researchers conclude that some chondrules must have been ‘remelted’ or partially ‘remelted’.

Because of the huge challenges for a naturalistic origin for chondrules, the origin of chondrites is a major mystery for astronomical science:

“Blobs called chondrules in the fabric of rocks from space have long baffled scientists. A new idea may shed light on their origins, but some experts have given up hope. ... How would you like your decades of research on a field’s central problem to be summed up by the statement that ‘these objects remain as enigmatic as ever?’”<sup>1</sup>

These challenges are better explained by God creating the solar system in a very short time, as described in Genesis.

## References

1. Psarris, S., What You Aren’t Being Told About Astronomy, vol. 1: Our Created Solar System, Creation Astronomy Media (DVD), 2009.
2. Psarris, S., What You Aren’t Being Told About Astronomy, vol. 2: Our Created Stars and Galaxies, Creation Astronomy Media (DVD), 2011.
3. Kerr, R.A., Meteorite mystery edges closer to an answer—or the end of a field, *Science* 341: 126–127, 2013.
4. en.wikipedia.org/wiki/Chondrule, accessed 10 November 2014.

# Changing-look quasars: how do they fit into a biblical creationist model?

John G. Hartnett

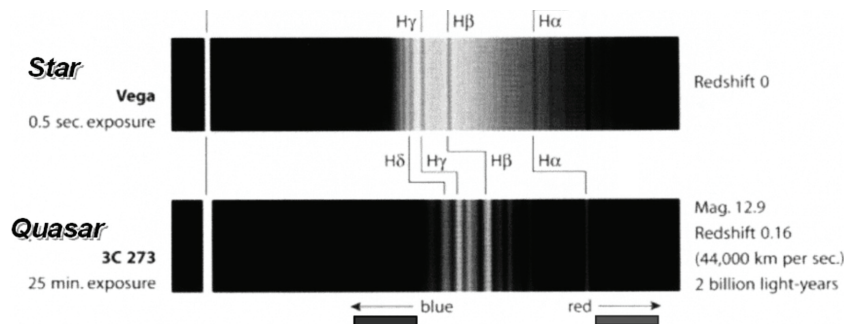
Quasars are very high redshift (figure 1) astronomical objects with broad emission line (BEL) spectra. The latter is very different to that in the usual ‘normal’ galaxies. This means the objects’ redshifts and BEL spectra can be used to identify them. And because of their high redshifts they are assumed to be very distant, very luminous active galaxies with super-massive black holes at their hearts, powering them to emit prodigious amounts of radiation over all wavebands of the electromagnetic spectrum.

Most of the high redshift objects in the universe are quasars. The redshifts of galaxies and quasars when interpreted within big bang cosmology—the greater the redshift the greater the distance—means that the most distant objects are seen at a time when the universe was youngest.<sup>1</sup> Following big bang thinking, quasars are then considered to be just galaxies

in some early stage of development—back closer in time to the big bang—than the usual spiral and elliptical galaxies we might see with much lower redshifts. The quasar 3C 273, shown in figure 2, the first to be identified (discovered in the early 1960s by astronomer Allan Sandage), has been shown to reside in a giant elliptical galaxy in the constellation of Virgo. According to standard cosmology, its redshift puts it at a distance of 2.5 billion light years from Earth.

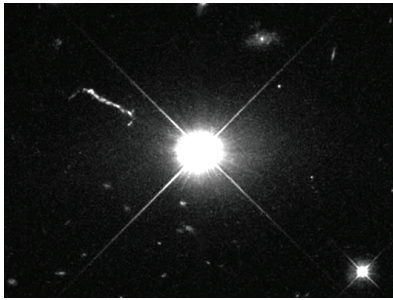
## Quasar to galaxy transitions

According to the big bang theory, how long should a quasar remain in the form of a quasar before transitioning into a normal galaxy and how long should that transition take? Quite obviously the answer to that question depends on one having a correct understanding of what quasars actually are and an accurate model describing their evolution. It would be no underestimate to state that an accurate model for galaxy formation, let alone a transition from a quasar to a normal field galaxy, is far from being known. The formation of a galaxy alone requires the invoking of a very large dark matter content and often ‘jumping over’ the important details of star formation just to obtain something that looks like a galaxy. This means there are physical laws in this universe that create barriers in computer simulations preventing the



**Figure 1.** Spectra of quasar 3C 273 compared to the star Vega. Spectral lines are shifted towards the red end of the spectrum, from which its distance is determined using the standard LCDM cosmology.





**Figure 2.** The quasar 3C 273, which resides in a giant elliptical galaxy in the constellation of Virgo

formation of stars and hence galaxies. It is these that must be ‘jumped over’ in order that the simulations may proceed.<sup>2</sup>

We can assume that quasars have masses comparable to that of most galaxies. From that it follows then that naturalistic changes—that is, uniformitarian changes—can be expected to be of the order of one billion years.<sup>3</sup> Without any real model for the changes expected in quasars, it may not be too unreasonable to expect any changes in their luminosity to be over uniformitarian timescales, and fuelled by growth of their super-massive black holes, as some propose.

By contrast, according to the Genesis 1 narrative, God took one 24-hour day to create all astronomical objects, therefore we expect at creation that the youngest sources (which could include quasars) have very quickly changing observable features, such as luminosity. Yet very rapid changes, even down to timescales of days and weeks, in the observed luminosity of quasars have been recorded.<sup>4,5</sup> One suggestion is that those variations are caused by microlensing<sup>6</sup> and another is obscuration by dust, but these mechanisms are considered to be too long.<sup>7</sup> Another is the rapid consumption of a passing star or gas and dust by the central supermassive black hole. Such proposals are offered because changes on such short timescales are not expected from the

growth of the alleged supermassive black holes at the heart of the quasars.

### Changing-look quasars

Now we read in an online news report<sup>8</sup> that astronomers think have detected a dozen quasars in a disappearing act—the so-called ‘changing-look quasars’. Or they have been caught transitioning into their quiescent and dimmer counterparts—galaxies with starving black holes at their cores. This fact has left astronomers asking whether these objects are shutting down permanently or simply flickering out for the time being.

“Last year Stephanie LaMassa from NASA Goddard Space Flight Center (then at Yale University) discovered the greatest change in luminosity ever detected in a quasar. She was digging through data from the Sloan Digital Sky Survey when she found that a quasar had dimmed in brightness by a factor of six in just 10 years. *Its spectrum changed, too, from that of a classic quasar to a regular galaxy* [emphasis added].”<sup>8</sup>

Because astronomers believe in the very long timescale big bang

paradigm they are forced to suggest any rapid dimming in the luminosity of any quasar must be either a transient effect or the very rare chance of observing the fuel exhausted from a supermassive black hole. One report states that:

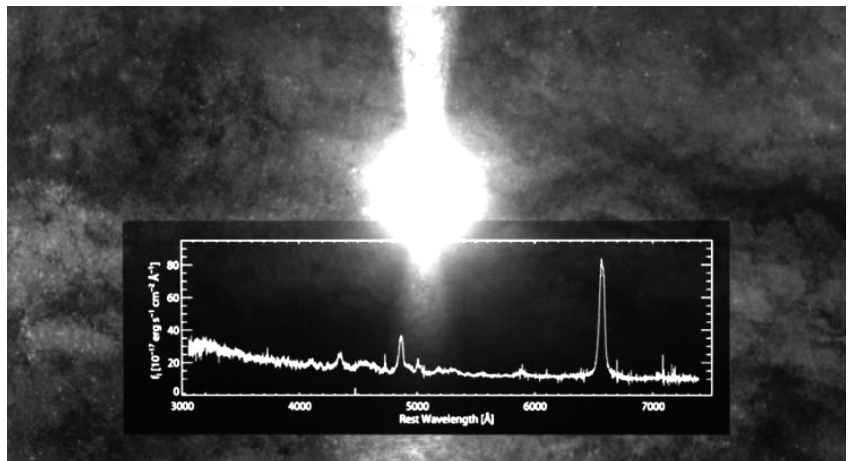
“Astronomers can’t find any sign of the black hole at the center of the quasar SDSS J1011+5442, and they couldn’t be happier.”<sup>9</sup>

In the case of this quasar (see figure 3) it is alleged that:

“... over the past ten years, it appears to have swallowed all the gas in its vicinity. With the gas fallen into the black hole, astronomers from the Sloan Digital Sky Survey (SDSS) were unable to detect the spectroscopic signature of the quasar, which *now appears as an otherwise normal galaxy* [emphasis added].”<sup>9</sup>

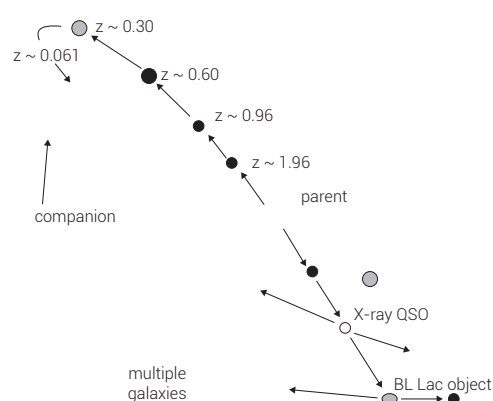
The dimming was very significant and now appears like a normal galaxy.

“‘The difference was stunning and unprecedented,’ said John Ruan of the University of Washington, lead author of a related paper ... ‘The hydrogen-alpha emission dropped by a factor of 50 in less than twelve years, and the quasar now looks like a normal galaxy.’ The change



**Figure 3.** The image shows an artist’s impression of the ‘changing-look quasar’ as it appeared in early 2015. The glowing blue region shows the last of the gas being swallowed by the central black hole as it shuts off. The spectrum is the previous one obtained by the SDSS in 2003. (Credit: Dana Berry/SkyWorks Digital, Inc.; SDSS collaboration).





**Figure 4.** Arp's model of ejection of quasars from active parent galaxies and their eventual change to normal galaxies. Reproduced from Hartnett<sup>11</sup> after Arp's original in his book *Seeing Red*.

was so great that throughout the SDSS collaboration and astronomy community, the quasar became known as a 'changing-look quasar' [emphasis added]."<sup>9</sup>

However, one of the newly discovered, rapidly dimming quasar did re-brighten.

"And one of the 12 newly discovered objects did *not just disappear but reappear [sic]*. Krolik thinks that this lonely quasar blazed back into existence for the same reason that it flickered out: a variation in the gas and dust flowing onto the black hole [emphasis added]."<sup>8</sup>

Certainly it is possible that the standard interpretation for quasars as AGNs<sup>10</sup> powered by a super-massive black hole is one possible explanation. *The next step then will be to see if any of the other newly discovered dozen or so quasars re-brighten over the coming years.*

### A different explanation

A different explanation is one consistent with the work of the late Halton Arp<sup>11</sup> where he suggested that quasars are born from the hearts of active parent galaxies. Over time, which he had no measure of, the ejected quasars transitioned from active, highly luminous, high

redshift objects with BEL line spectra to the usual field galaxies with much lower redshifts and typical spectra. This is illustrated in figure 4. Quasars are ejected in opposite directions from the nucleus of an active galaxy and over time they change their internal state including redshift, which decreases with finite discrete steps towards the commonly observed low redshift in field galaxies. Thus quasars and active galactic nuclei become normal galaxies.

Apparently the idea that quasars or active galactic nuclei could become inactive is not controversial in the big bang universe. But the expected timescale is not less than tens of thousands of years. What LaMassa and her colleagues doubted was that a quasar could go from active to inactive in just 10 years. But this is what these newly discovered, rapidly dimming quasars have established. Rapid changes in the emission properties of the quasars, on timescales very much in line with a creation scenario, are observed. Even their spectra changing from that of a classic quasar to a regular galaxy.<sup>9</sup>

### A biblical creation explanation

So this discovery is consistent with a creation scenario where we expect processes in astronomical sources to be well less than 7,000 years. In the case of a creation process of galaxies formed from AGNs—the parent galaxies—and the ejected galaxies in the form of quasars, it would be essential that the quasars (at least some of them) have changed to normal galaxies in a period less than the time since Creation, that is less than about 6,000 years.

However, it is also expected that many galaxies were created in their

current forms, but if Arp's evidence for quasars and active galactic nuclei transitioning to normal galaxies is correct, then this is what would be expected in the biblical Creation model. Here we have an opportunity to see if these rapidly dimmed quasars remain dim or re-brighten. Time will tell.

### References

1. This claim I dispute, as there is evidence that puts this idea in doubt, [johnhartnett.org/2014/01/01/galaxy-quasar-associations/](http://johnhartnett.org/2014/01/01/galaxy-quasar-associations/). There is strong evidence, even in the very large galaxy surveys, that suggests a very high probability of high redshift quasars being associated with low redshift parent galaxies.
2. Hartnett, J.G., Stars just don't form naturally—'dark matter' the 'god of the gaps' is needed, [creation.com/stars-dont-form-naturally](http://creation.com/stars-dont-form-naturally), September 2015.
3. Back of the envelope calculation for the formation of a typical-sized galaxy and hence quasar from the free collapse of a proto-Galactic cloud is of the order of one billion years. See Carroll, B.W. and Ostlie, D.A., *An Introduction to Modern Astrophysics*, 1<sup>st</sup> edn, pp. 1074–1075, 1996.
4. Hawkins, M.R.S., Time dilation and quasar variability, *Astrophys. J.* **553**:L97–L100, 2001.
5. Hawkins, M.R.S., On time dilation in quasar light curves, *MNRAS* **405**:1940–1946, 2010.
6. When a quasar is sufficiently aligned with a massive compact foreground object the bending of light due to its gravitational field is distorted, resulting in an observable magnification. The timescale of the transient brightening depends on the mass of the foreground object as well as on the relative proper motion between the background 'source' and the foreground 'lens' object.
7. MacLeod, C.L. *et al.*, A systematic search for changing-look quasars in SDSS, *MNRAS* **457**(1):389–404, 2016.
8. Hall, S., The Case of the Disappearing Quasars, *Scientific American*, [scientificamerican.com/article/the-case-of-the-disappearing-quasars/](http://scientificamerican.com/article/the-case-of-the-disappearing-quasars/), 23 November 2015.
9. Raddick, J., The Case of the Missing Quasar, *SDSS*, [sdss.org/releases/the-case-of-the-missing-quasar/](http://sdss.org/releases/the-case-of-the-missing-quasar/), 6 January 2015.
10. AGN = Active Galactic Nucleus
11. Hartnett, J.G., The heavens declare a different story, *J. Creation* **17**(2):94–97, 2003.

# Vitalism dusted-off as a 'solution' to evolution's fatal problems

***Evolution 2.0: Breaking the Deadlock Between Darwin and Design***

Perry Marshall

BenBella Books, Dallas TX, 2015

John Woodmorappe

Author Perry Marshall comes from an unusual background, for someone who studies evolution-related issues. He is not a biologist; however, his bibliography shows that he has an extensive knowledge of biology. In addition, he has tested his knowledge in online debates with evolutionists.

The author is a computer specialist who specializes in coded information. He gives many examples of coded information in this book, and does so in a lucid manner. Language is a form of code. Computers obviously depend upon code. DNA contains code. Marshall emphasizes the inability of biological information to arise spontaneously.

In a somewhat dramatic way, the author warns that the reader will be made uncomfortable by reading this book—be he an evolutionist or a creationist. As soon becomes evident, the drumbeat is unwarranted.

It soon becomes obvious to the informed reader that Marshall gives too much credit to certain developments of evolutionary theory, most of which are mundane, most of which have been known for a fairly long time, and none of which, upon close examination, substantially enhance the evidentiary basis for

presumed molecules-to-man evolution. This includes such phenomena as transposons, gene duplications, hybridization, epigenesis (neo-Lamarckism), horizontal gene transfer, accelerated mutation rates, and rapid speciation.

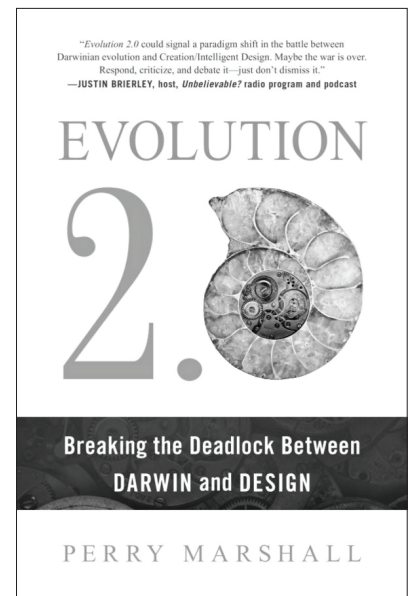
Marshall was once a young-earth six-day creationist (pp. 190, 248, 265). He now rejects creationism in large part because of what he thinks is the overwhelming evidence for an old earth. However, nowhere in the book does he show any hint of understanding the flaws of long-age dating methods or the evidences for a young universe. He now accepts evolution, while professing to be open minded to Divine intervention. It turns out, however, that he is holding to a confusing and contradictory mixture of evolutionary and teleological concepts.

## God or no God? Straddling the middle

Marshall takes a “pox on both your houses” approach towards both hard-nosed evolutionary atheists, and creationists as well as proponents of ID (Intelligent Design). He quips:

“The neo-Darwinists deny purpose, even though their language drips with purpose-laden terms like ‘selfish genes’. They criticize young earth creationists for insisting the Earth only *appears* to be millions of years old ... yet they claim that living things only *appear* to be purposeful. What’s the difference [emphasis in original]?” (p. 246).

However, informed YECs deny that the earth appears that old; age



has no appearance *per se*, but is the *interpretation* of certain appearances.

Marshall faults evolutionists for glossing over the insurmountable problems involving the supposed spontaneous origin of biological information. At the same time, he accuses ID proponents of being too quick to invoke a Designer.

In essence, Marshall believes that both sides are non-objective when dealing with God. One side invokes God for unsolved mysteries, while the other side discounts Him out of hand. Thus, to Marshall, the ‘god of the gaps’ has an evil twin, “God had nothing to do with it”.

Pointedly, the author rejects the standard ‘scientific’ position that God is outside of the realm of science. He comments:

“Every philosopher knows science cannot prove God. Hopefully, most scientists know this, too. But science’s intrinsic limitations don’t mean that God doesn’t exist ... Since science always relies on philosophical and metaphysical assumptions that lie outside of science, it is intellectually dishonest to ban debates about God and origins from the classroom

just because God cannot be scientifically tested” (p. 75).

Marshall believes that God and evolution can be reconciled if only both sides simultaneously embrace God and naturalistic processes, while letting free inquiry determine the limits of both. He elaborates:

“If, however, we take ‘Designer’ to be an *ultimate* explanation, with an unknown number of layers in between, then both nature and God receive their due respect. Science is freed from the corset of reductionism, and scientists gain greater reasons to pursue ambitious research programs [emphasis in original]” (pp. 213–214).

The foregoing sounds nice, but really offers nothing different from what is already going on anyway. The ID proponent generally believes that most of the layers of naturalistic explanations, for once-mysterious biological phenomena, are already known. For this reason, a designer is *not* a ‘god of the gaps’ copout.<sup>1</sup> Instead, the designer is a viable explanation for the remaining crucial biological mysteries, such as the origin of life. The evolutionist, on the other hand, believes that all the layers will eventually prove to be naturalistic, and so the Intelligent Designer is, or will be, squeezed out of existence.

Finally, Marshall’s formulation turns out to be a tautology, and a trivial one at that. If ‘designer’ just means ‘ultimate explanation’, then, by definition, the ‘designer’ must exist. Whatever made the universe is the ‘designer’. To the evolutionist, the ‘designer’ is nothing more than the blind evolutionary process itself. In fact, Marshall’s formulation turns out to be identical to the parallel redefinition of God, only using different words. If ‘God’ means ultimate reality, then, by definition, ‘God’ must exist. If a Supreme Being exists, and made the world, then He is the ultimate reality, and He rightly is called God. However, if naturalistic

evolution is ultimate reality, then, by definition, naturalistic evolution is ‘God’.

### ‘Bad design’ in nature?

The author adopts a middle view on so-called suboptimal structures. On one hand, he provisionally accepts certain suboptimal structures, and adheres to the premise that the evolutionary process makes designs that are, in his words, ‘best guesses’. On the other hand, he realizes, from personal experiences that he elaborates on, that “Designs always have delicate tradeoffs” (p. 231).

Pointedly, Marshall chides evolutionists for their intellectual hubris in their dysteleological arguments. He warns that:

“But human beings must be very careful not to proudly assert that we could ‘obviously do better’. We don’t know that. We do not understand what’s involved in designing an eye because we’ve never built one. (Or, actually, we have, and they’re all inferior.) If you lose your eye, there’s not a single scientist in the world who can build you a new one. Especially not arrogant speculators who try to tell you why the design of the eye is ‘pathetic’. If I were selecting an eye surgeon, I’d look for one who has deep respect for the human eye, not disdain for it. How about you?” (p. 231).

### Defending evolution on dubious grounds

The author is enamored with the ‘shared mistakes’ argument involving human and ape pseudogenes. In doing so, he shows not a hint of understanding of alternative explanations for this fact,<sup>2</sup> or of recent discoveries of functionality among pseudogenes.

Some of the author’s ideas appear to elevate relatively unimportant phenomena into ones of great (imagined) evolutionary significance. For instance, the author brings up rapid speciation. However, this is an example of ‘horizontal’ variation and not the origin of biological novelty. Informed creationists, both before and after Darwin, accepted speciation, so it’s hardly a unique evolutionary insight. Much the same applies to hybridization.

Now consider epigenesis, which is also called neo-Lamarckism, and which involves the parents’ transmission of traits to their descendants outside of the transmission of genes. As an example of epigenesis, Marshall cites the Dutch parents who, having starved during the German occupation in WWII, had children that were smaller in size. However, it is unclear how many different traits can be transmitted through epigenetic processes, and for how many generations this extragenic inheritance can be operative. In addition, if the real issue is not ‘survival of the fittest’ but ‘the arrival of the fittest’, then the exact mode of transmission, from generation to generation, is of little importance. Most important of all, it is unclear if epigenesis plays any significant role (or any role at all) in the supposed spontaneous origin of biological information.

Much of the author’s reasoning does not solve evolutionary problems, but rather begs the question. As a classic example of question-begging, think of the ‘solution’ to origin-of-life problems that posits that life arose on another planet. To say that the origin-of-life mystery is solved by its appearance on another planet begs the question about its origin on *that* planet. In assuming what it needs to demonstrate, it only relocates the problem from Earth to another planet.



Marshall does not bring up the foregoing argument. However, he engages in analogous forms of question-begging and problem-relocation pro-evolutionary arguments. Let us consider some of them.

The author accepts, with not so much as a glimmer of questioning, the serial endosymbiosis theory. According to this theory, for example, the mitochondrion was once a stand-alone cell before it became engulfed by the bacterial cell, and relegated to its present role of a “powerhouse” organelle. However, this raises the question about how even the stand-alone mitochondrion originated.

Now consider gene transfer in bacteria. Marshall claims that this shows how rapidly evolution can occur, as, for example, the emergence of ‘superbugs’ that are resistant to antibiotics. It does not. The capability to resist certain antibiotics is not being created: it is merely being ‘passed around’ from one bacterial cell to another. The author’s contention begs the question about how the resistance to antibiotics originated.

Marshall repeats the argument that the bacterial flagellum is not a compelling example of irreducible complexity, as the bacterium could have imported much of the ‘machinery’ from other bacteria, using processes comparable to horizontal gene transfer. However, this only relocates the problem, and begs the question on the origin of this ‘machinery’ itself.

The author brings up gene duplication as a factor in evolution. However, this begs the question about how the original gene arose in the first place.

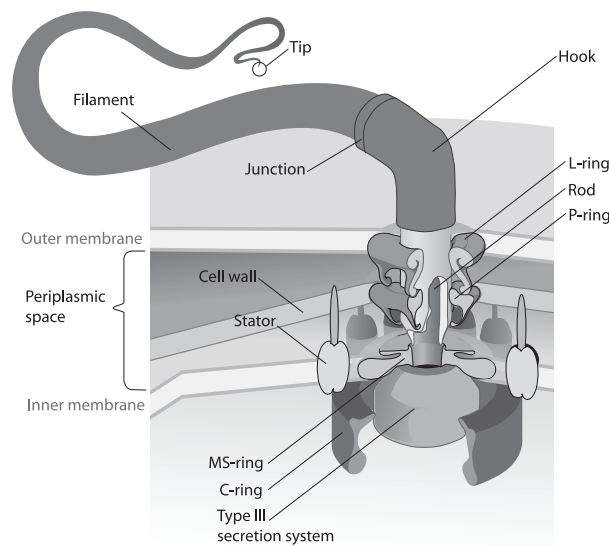


Figure 1. Bacterial flagellum

### What is a mutation?

Marshall appears to think of a mutation as the change of a single nucleotide in the DNA molecule. Labouring under this misconception, the author expresses wonder at genomic changes caused by transposons, gene duplication, etc. Far from being some kind of new or game-changing fact, as Marshall seems to think, these have been known by evolutionists for decades. Nor do they render obsolete the neo-Darwinian synthesis: they merely expand its scope. Finally, they do not solve the central problem of *all* evolutionary theories, which is the origin of novel, functioning biological systems.

### Conflating non-randomness with intentionality

The author’s thinking, while superficially impressive, appears to be a confusion of distinct phenomena. Let us first define some terms to make this clear.

Randomness simply means having an equal probability. For instance, suppose that a bag contains 851

beans, and a person is asked to blindly pick one bean out at random. If his choice is truly random, then each bean has an equal probability of being picked; that is, 1 chance in 851. However, what if the person, unwilling to possibly spill some beans, is disinclined to bury his hand deeply in the bag? Beans near the top of the bag now have a relatively high probability of being chosen, while those near the bottom have almost zero probability of being chosen. His choosing of a bean is now clearly non-random.

To distinguish non-randomness from intentionality, let us consider another scenario. This person (still disinclined to reach for the bottom beans) has a preference for beans that are rough to the touch. His choice is therefore now governed not only by non-randomness but also by intentionality.

As intentionally becomes a sustained behaviour, it grades into teleology. Teleology means a goal-oriented intentionality, an intentionality that has a pre-determined outcome. Let us suppose that this same person picking out the beans is determined to remove as many rough-skinned beans as possible. His choice of beans is not only non-random, and not only governed by intentionality, but is unmistakably teleological in nature.

### The intentionality of evolution?

The author speaks of classical neo-Darwinism thought largely in terms of random mutations. He argues the fact that mutations are non-random. However, this means little, and confuses the issue. It would be better

to think of ‘intentional’ mutations. His confusion is evident by his conflation of the two, as he writes, “Mutations aren’t random; they’re goal directed” (p. 259). How so? One must not confuse outcomes with intentionality, but that is what Marshall appears to be doing.

Let us illustrate the author’s confusion, of outcome and intentionality, by considering gravity. We could say that gravity prevents the earth itself, earth’s objects, and the earth’s atmosphere, from uselessly drifting off into interstellar space. While this is an outcome, it is not intentionality. Gravity has no way of ‘knowing’ that its operation is in any way related to its Earth-preserving effects. Thus there is no way that gravity is acting according to intentionality. In addition, if one does not believe in God, one cannot suppose that gravity came into existence because of someone’s intention of maintaining a functional earth.

Marshall seems to misunderstand retrotransposition as some kind of intentional process which operates according to the needs of the organism. It does not. It merely enhances variability, which allows natural selection to act on a larger set of mutational ‘trials’.

In like manner, Marshall seems to think that accelerated mutation rates are teleological. They are not. They are simply the outcome of environmental stressors acting on the genome. They do not have intentionality, as they have no way of ‘knowing’ that organisms are now facing increasing challenges owing to the stressful environment.

There is no evidence, certainly none supplied by the author, that ‘intentional’ mutations exist. Finally, Marshall demolishes his own argument as he makes the following revealing statement, “Factors we don’t yet understand influence mutation rates of cells, and mutations maximize

the changes of survival” (p. 111). Since, and by his own admission, we do not understand the causes of mutation rates, then most certainly we cannot even begin to suggest that they are intentional in any way—even if they theoretically could be!

### Vitalism making a comeback?

Author Perry Marshall flirts with a teleological conception for the presumed disappearance of legs in the course of whale evolution (figure 1). He suggests that the (alleged) retention of the ability of the whale genome to encode for legs implies either (or both) the fact that the presumed vestigial bones still serve a function, or that

“... the adaptive program was trying to hang on to valuable inventory. It seemed almost ... conservative. As though it knew it might need those legs sometime in the future, and so resisted deleting them” (p. 15).

This is evolutionistic teleology with a vengeance!

The author is reviving century-old discredited ideas. Bergsonism, or vitalism, posits that living things have some kind of ‘drive’, or predetermined ‘plan’, to evolve, and to evolve towards certain pre-specified outcomes. His idea would only make sense if the processes which govern the expression of whale genes had some mysterious way of predicting the descendant-whales’ needs in the distant future, and then had some way of conducting themselves according to these foresights!

### Introduction to coded information

The author utilizes his background in computers to illustrate how codes, and coded information, work. Coded information uses a language called ASCII. In ASCII, the letter ‘A’ is encoded by ‘1000001’. When one

presses the letter ‘A’ in the keyboard, it is encoded as ‘1000001’. The computer then decodes the ‘1000001’, and the letter ‘A’ is displayed on the screen.

In like manner, the DNA contains code. GGG (guanine-guanine-guanine) is not the amino acid glycine. It is encoded information for the ribosomes to *add* glycine at that spot in the encoded protein. Before that, the coded information is encoded into messenger RNA, and then decoded using matching transfer RNA to make the amino acid glycine. In other words, GGG are symbolic instructions to make glycine. In addition, in those parts of the DNA molecule that are not involved in protein synthesis, GGG does not mean glycine, and may mean something different, or even nothing at all.

### Biological encoding and the origin of life

Basing his thinking on his background in computer information systems, notably the role of codes, Marshall is mercilessly critical of evolutionary origin-of-life hypotheses. He writes:

“In this book, I do not even consider the question of what kind of process it might have taken to physically build even a ‘simple’ cell with enough parts to function. All cells have hundreds of thousands of moving parts. I have attempted only to consider the question of how the instructions for the daughter cell got into the DNA, and how the language for those instructions was formed. Answers to even that simple, obvious question proved elusive” (p. 179).

The author then focuses on the specifics of how evolutionistic origin-of-life ideas utterly fail to explain the presumed spontaneous origin of coded information. For example:

“Many books and papers on the Origin of Life only discuss

the assembly of the chemicals themselves. Nothing we know about chemicals tells us where the codes come from” (p. 181).

“A code will only function in the context of an encoder and decoder. Plus, amino acids aren’t code. A string of nucleotides all by itself is not a code. Chemicals all by themselves don’t communicate. No one has ever demonstrated that chemical reactions alone can generate codes ... . Without code there can be no self-replication. Without self-replication you can’t have reproduction. Without reproduction you can’t have evolution or natural selection” (p. 182).

“Codes are not matter and they’re not energy. Codes don’t come from matter, nor do they come from energy. Codes are information, and information is in a category all by itself” (p. 187).

### The untenable RNA-only biological world

Marshall is unsympathetic to the evolutionist speculation that RNA came first, and that DNA was a later evolutionary add-on. He comments:

“There are problems with the RNA world hypothesis: (1) many scientists believe RNA is too complex to have arisen without the presence of the very same life forms it is believed to have created;

(2) RNA is inherently unstable, so even if it did arise, it wouldn’t last long without a cell to protect it; (3) catalysis of chemical reactions is seldom observed to occur in long RNA sequences only; and (4) the catalytic abilities of RNA are limited. The RNA world hypothesis doesn’t actually solve the chicken-and-egg problem of RNA and proteins: You need RNA to produce proteins, and you need proteins to build the machinery to read the RNA in the first place” (p. 181).

### The Second Law of Thermodynamics

Although Marshall does not mention the Second Law of Thermodynamics by name, he alludes to the fact that it virtually prevents the spontaneous origin of biological information. Pursuing his earlier example of computers further, Marshall adds that

“Nothing we presently know in pure physics or chemistry explains the origin of these cellular engineering capabilities. We don’t know how cells make choices. If the universe booted up the first cell without the action of a designer, then the universe itself must possess directional qualities that nobody yet comprehends. Humans make machines. To date, we’ve never made self-replicating machines.

The closest we’ve come is computer viruses. But what if someone built a computer that reproduced other physical computers? What if someone wrote a computer program that got better and better with time, all by itself? What if Bill Gates started with DOS and we got the latest version of Windows without any human programmer ever having to write a line of code? That would be pretty impressive, wouldn’t it? We all know that human-made machines don’t evolve all by themselves; left to themselves, our cars and computers and PlayStations degrade and crash and break” (p. 151).

The author brings up Stanford computer scientist John Koza, who created programs that design analog circuits, thereby producing something new and valuable from scratch. However, Marshall points out that the program worked only because it imposed a very specific narrow set of constraints, and precise goals, in advance (p. 222). It was therefore a manifestation of design, and hardly a manifestation of quasi-spontaneous useful information originating by itself.

### Dawkins’ Weasel debunked

Arch-atheist Richard Dawkins wrote a computer program that generated random letters. The program was designed to change the letters, each time comparing the result with the goal—the classic phrase, *Methinks It Is a Weasel*. It took 43 iterations for the program to come up with this phrase, letter-perfect. From this, Dawkins has waxed in evolutionistic triumphalism, proclaiming that he has now decisively shown that no intelligent designer is needed for the origin of complex biological systems.

Dawkins’ claim is patently ridiculous. Marshall comments:

“But don’t forget—Dawkins has always insisted that evolution

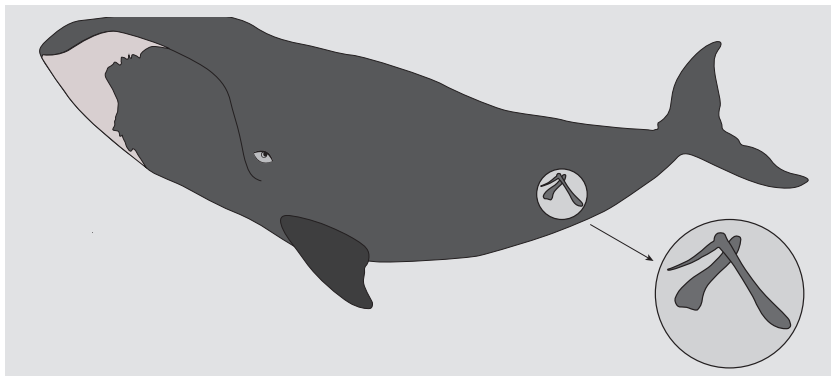


Figure 2. The so-called vestigial leg bones in the whale



is blind and purposeless. His program is anything but blind and purposeless; its goal is precisely defined from the beginning! What Dawkins actually proved with this experiment was: If you want to evolve, you have to start with a goal” (p. 222).

In other words, and ironically, Dawkins is using teleology in order to try to refute teleology!

### Conclusions

Marshall appears to be confused in his thinking. He even comes across as being somewhat mixed up in his thinking. For instance, he believes that evolution is teleological (as in the emergence of biological order) and, simultaneously, non-teleological (as in the case of certain so-called suboptimal structures). In fact, the author seems to misunderstand certain evolutionary processes (e.g. accelerated mutation rates) by endowing them with properties of intentionality that they do not have. The author is indecisive in his admittance of God into the picture.

The author’s tendency is to pick and choose parts of the evolution and creation arguments. His position is nothing new, and is unlikely to impress either camp. Contrary to the promises of the title of this book, it does not even begin to break the deadlock between Darwinism and design.

### References

1. Compare Weinberger, L., Whose god? The theological response to the god-of-the-gaps, *J. Creation* 22(1):120–127, 2008; creation.com/gaps.
2. Woodmorappe, J., Are pseudogenes ‘shared mistakes’ between primate genomes? *J. Creation* 14(2):18–30, 2000.

## Justifying Christian belief

### *Apologetics: A Justification of Christian Belief*

John M. Frame

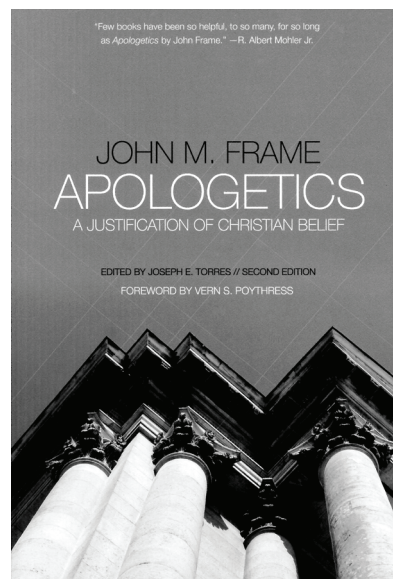
P&R Publishing, Phillipsburg, NJ, 2015

Lita Cosner

The serious apologist must think seriously about what apologetics is, what it is trying to accomplish, and how it intersects with evangelism. John Frame’s 20<sup>th</sup> anniversary edition of *Apologetics: A Justification of Christian Belief* does a good job of introducing a form of presuppositional apologetics thoroughly.

The main text is 288 pages (not counting foreword, introductions, glossary, indices, or bibliography, which add another 81 pages) and it is written at a level suitable for use in a college or seminary classroom. However, it should be accessible to pastors and laypeople who are serious about studying apologetics. Frame does a good job of defining his terms and making his ideas accessible to the average person, though the footnotes that often take up a substantial portion of the page can be daunting at times.

*Apologetics* is useful as a thorough introduction to the Van Tilian school of apologetics, i.e. that of Cornelius Van Til (1895–1987), a founding professor of Westminster Theological Seminary and a minister in the Orthodox Presbyterian Church. But even those who disagree with his particular school should find elements which are useful. It is so wide-ranging that this review will focus on the main body of the book and not on the appendices, which provide useful peripheral data but which are ultimately optional reading.



### Presuppositional apologetics

Frame is an unapologetic advocate of presuppositional apologetics from a Calvinist standpoint, but those who do not share his Reformed theology should still be able to gain valuable insights from the text. From him, presuppositional apologetics is simply assuming the Bible is true, and refusing to cede that fact for the sake of argument in dialoguing with those who disagree. “If we adopt the Word of God as our ultimate commitment, our ultimate standard, our ultimate criterion of the truth and falsity, God’s Word then becomes our ‘presupposition’” (p. 3). He disagrees that we can ever dialogue on a neutral basis:

“To tell the unbeliever that we can reason with him on a neutral basis, however that claim might help to attract his attention, is a lie. Indeed, it is a lie of the most serious kind, for it falsifies the very heart of the gospel—that Jesus Christ is *Lord*. There is no neutrality” (p. 8).

Some people argue that pre-suppositional apologetics is circular. Frame responds:

“It sounds circular to say that our faith governs our reasoning and also that it in turn is based on rationality. But it is important to remember that the rationality of which we speak, the rationality that serves as the rational basis for faith, is God’s own rationality. The sequence is as follows: God’s rationality → human faith → human reasoning. The arrows may be read ‘is the rational basis for’. So in this sense, the sequence is linear, not circular” (p. 10).

However, this has been criticized by some because the real conclusion is back to God’s rationality, so the argument is still circular.<sup>1</sup>

Furthermore, everyone must use this sort of ‘circular’ thinking because: “... when one is arguing for an ultimate criterion, whether Scripture, the Qur’an, human reason, sensation, or whatever, one must use criteria compatible with that conclusion. If that is circularity, then everyone is guilty of circularity” (p. 11).

But this isn’t necessarily the case; circular thinking only arises when we try to prove presuppositions with those presuppositions. However, presuppositions are by definition not provable because they are the *beginning point* of our thinking.

### General or natural revelation

While Scripture is our ultimate authority, Frame does not believe this prohibits Christian apologists from using arguments from outside of Scripture. This is because God has revealed Himself in creation (Romans 1).

“Natural revelation is every bit the word of God and absolutely authoritative. The difference is that Scripture is a verbal divine utterance that God gives us to

supplement and correct our view of his world. We must humbly accept that assistance. In doing so, we do not make Scripture more authoritative than natural revelation; rather, we allow the Word (with its ever-present Spirit) to correct our *interpretation* of natural revelation” (p. 22).

One criticism of this view is that “word of God” necessarily implies propositional revelation, which general revelation is not.<sup>2</sup> However, he rejects the common ‘two books’ view which in effect makes nature a 67<sup>th</sup> book of Scripture:

“That sort of argument has been used to justify relatively uncritical Christian acceptance of evolution, secular psychology, and so on. In such arguments, Scripture is not permitted to do its corrective work, to protect God’s people from the wisdom of the world (See 1 Cor. 2: 6–16)” (pp. 22–23).

### The message of the apologist

Frame presents Christianity as a philosophy that can compete successfully against materialism, empiricism, and other philosophies because it contains all the essential elements of a worldview. In addition, Christianity has a number of unique advantages as a philosophy. Frame presents the idea of God as the Absolute Personality behind the universe, in contrast to the impersonal absolutes presented by atheistic philosophies. Assuming an Absolute Personality allows one to speak of meaning and rationality inherent in the universe. He says:

“The Christian apologist should lay more emphasis than did Cornelius Van Til on the issue of impersonalism vs personalism. It is this issue, as we have seen, that distinguishes the Christian worldview from all others” (p. 39).

If God created the universe, then we should expect the universe to

reflect aspects of His being and nature. Frame shows how the universe implies a sovereign God and even the Trinity.

### Faith and evidence

Van Til argued that there is absolutely certain proof for the existence of God, but the sort of proofs that most apologists present fail to convince unbelievers—at least for as long as they remain unbelievers. Frame deals with this by revising the concept of proof by saying not only does it have true premises and sound logic, but that it *ought* to be persuasive.

But Frame notes that Scripture rebukes those who demand proof for God’s existence—it states that God is clearly revealed but does not argue as such for His existence. And since God created and sustains everything, nothing is properly understood apart from Him. For most, the problem is not genuinely intellectual but rather sinful rebellion.

On the other hand, many are content to believe in God without proof of His existence, and Frame notes that Scripture praises childlike faith. But apologists must be ready to answer those who demand evidence for His existence.

Frame argues that there is no such thing as a genuine atheist because God has revealed Himself to everyone. However, people suppress this knowledge by ignoring and disobeying God. It is valid to appeal to this suppressed knowledge in our interactions with unbelievers.

### The transcendental argument for the existence of God

Van Til popularized the ‘transcendental argument’ for the existence of God: in short, logic demands the existence of God.

“God is logically necessary in the sense that without him, the use of

	Van Til	Frame
<b>Proof</b>	There is “absolutely certain proof” for Christian theism.	We need to distinguish between the certainty of evidence for Christian theism (which is absolute) and our human arguments (which are fallible and often uncertain).
<b>Neutrality</b>	All reasoning must presuppose divine revelation. Reasoning is never religiously neutral.	I agree with enthusiasm.
<b>Presuppositions</b>	All reasoning must presuppose the absolute-personal Trinitarian Lord who exercises total and absolute control over his creation.	Again, I agree with enthusiasm.
<b>Antithesis and common grace</b>	Our reasoning must take into account both the noetic effects of sin and the restraining influence of common grace.	I agree, but nuance is needed.
<b>Suppression</b>	The unbeliever suppresses the truth by a dialectic of rationalism and irrationalism.	Agreed.
<b>Evidence</b>	We may freely use logical arguments and present evidences for the truth of Scripture. But we shouldn’t do this ‘endlessly’ without challenging the unbeliever’s philosophy of fact.	Agreed, with the proviso that we be permitted to vary our approach based on the nature and questions of our audience. We don’t always need to explicitly speak of epistemology.
<b>Proving Christian theism</b>	We should always seek to prove Christian theism ‘as a unit’.	Yes ... but. To some extent it is legitimate to prove one fact about God at a time, being careful not to distort the whole in expounding the parts.
<b>Certainty or probability?</b>	Our arguments should always claim absolute certainty, never mere probability.	See the first point above. It is legitimate in some cases, and even unavoidable, to use arguments that claim only probability.
<b>Should we ‘supplement’ the unbeliever’s knowledge?</b>	We should not produce arguments that merely “supplement” the unbeliever’s knowledge. We should seek to overturn the very foundations of his thought.	If we reject an extreme view of antithesis, we must recognize that there will be elements of truth in unbelieving thought. This is not to deny the importance of overturning the foundations of unbelieving thought, for elements of truth in unbelieving thought are at variance with its foundational commitment.
<b>Direct or indirect arguments?</b>	A truly transcendental approach is indirect rather than direct.	Any indirect argument of this sort can be turned into a direct argument by some creative rephrasing. If the indirect form is sound, the direct form will be too—and vice versa.

Figure 1. Table reproduced from p. 94

logic would be impossible. He is the source of all order in the world and in the human mind, including logical order” (p. 70).

Atheists would argue that they can use logic perfectly well without the existence of God, but the point is that they have no *explanation* for logic apart from God. That is, natural selection would only select for survival value, not necessarily for logical thought.

Ethics also demands the existence of God—in fact, every ethical system

assumes there is an absolute ethical standard to which we all are subject. But as Frame points out:

“... secular theories cannot show why moral standards *obligate*. ... Moral standards can be obligatory only if their source is a *person* who *deserves* absolute obedience and reveals his will to human beings” (p. 72).

And only the God revealed in the Bible fits that standard. This does not mean that atheists do not have ethical

systems, but they have no adequate foundation for those moral principles. Even science demands the existence of God because it assumes an orderly universe in which scientific tests can be performed.

Frame differs with Van Til’s strategy regarding the use of the transcendental argument, however, in that he is willing to pair it with more traditional apologetic arguments such as the cosmological argument. He also differs with Van Til’s apologetic



method in some important respects, which he summarizes in a table, reproduced in figure 1.

### Arguing against atheism and agnosticism

Frame presents examples of how to prove God's existence. In answering agnostics, he simply observes that if anyone were *truly* unsure about whether God exists, one would expect them to 'hedge their bets' or seek after certainty one way or another. However, in practice most of them are indistinguishable from atheists, so can be addressed using the same general arguments.

Frame recommends using the moral argument against atheists—we all act and think as if our moral values are not subjective but objective. And he identifies truth as an ethical value: "The truth is what we ought to believe and what we ought to speak with one another. And these *oughts* are *oughts* of ethical value" (p. 100). Furthermore, subjective ethical statements are always self-contradictory because the atheist cannot logically state that there are absolutely no absolutes, and so on. Using the moral argument, the apologist can also point to the Ultimate Personality argument summarized above.

Frame finishes the chapter by evaluating many of the classic arguments for God, including the teleological argument, the cosmological argument, and the ontological argument.

### Proving the Gospel

Frame's chapter on Scripture is an excellent overview on why Christians should be confident about the authority and reliability of Scripture. Frame begins with Scripture's own doctrine of itself—i.e. Scripture claims to be the Word of God and speaks with the authority we would expect such a book to command. Liberal<sup>3</sup> scholars who

reject the supernatural inspiration of Scripture do not have any good reason to do so; rather, they reject Scripture's divine inspiration *a priori* because of anti-supernaturalist presuppositions. In fact, many liberal pronouncements about Scripture (such as claims about late composition) have had to be rescinded as new evidence has come to light vindicating Scripture. There are several lines of evidence Frame lays out to defend the divine inspiration of Scripture, including the argument from prophecy, New Testament miracles, and the Resurrection of Jesus.

### The problem of evil

Frame examines many attempted solutions to the problem of evil and finds them wanting. He critiques the idea of evil as illusion, the claim that the best possible world is one in which evil exists, and the defence that God is not the *proximate* cause of evil, as well as others.

Rather, he argues that Scripture gives us a definite answer regarding natural evil in that natural evil was caused by man's sin. Furthermore, we cannot accuse God of injustice because we are not in a position to judge Him.

### Comments on evolution

Frame comments a few times on evolution as an excuse some use for rejecting Scripture and gives his reasons for rejecting evolution as an explanation for life on earth. Genesis clearly teaches the creation of distinct 'kinds' of creatures and a special creation of Adam (who he takes to be the historical first man). His understanding of the limitations of natural selection is also noteworthy. There is only one comment in the book that would suggest his views on the age of the earth—unfortunately this seems to show that he accepts the evolutionary timescale. He says: "it

is not clear that being logical always or even usually preserves life; after all, cockroaches have inhabited the world much longer than man" (p. 111). Fortunately, he does not attempt to use compromise on timescale as a way to make Christianity more intellectually respectable as some do.

### A useful primer

Many people who study apologetics are 'disciples' of a particular teacher, and Van Til enjoys a substantial following. Frame stands firmly in the Van Til school, but with some important caveats that greatly improve the usefulness of his apologetic.

The greatest strength of Frame's apologetic is that he unapologetically stands on the authority of Scripture and refuses to cede that ground in the context of speaking with unbelievers. His responses to some common apologetic arguments that fall short are also very useful. This volume is a useful explanation of Van Til's apologetic that will be of interest to those of the same viewpoint or who want to know more about it.

### References

1. Beisner, E.C., *Classical Presuppositional Apologetics: Re-introducing an Old Theme*, 2001, revised 2006, [ecalvinbeisner.com/freearticles/ClassPresup.pdf](http://ecalvinbeisner.com/freearticles/ClassPresup.pdf).
2. See Kulikovsky, A.S., Scripture and general revelation, *J. Creation* 19(2):23, August 2005.
3. Frame defines liberal theology as "all theology (including so-called neo-orthodoxy) that does not accept the final authority of Scripture" (p. 133, note 9).

# The universe and the reality of its creator

## ***The Singular Universe and the Reality of Time: A Proposal in Natural Philosophy***

Roberto Mangabeira Unger, Lee Smolin

Cambridge University Press, UK, 2014

## ***Time Reborn: From the Crisis in Physics to the Future of the Universe***

Lee Smolin

Mariner Books, Bel Air, CA, 2014

John G. Hartnett

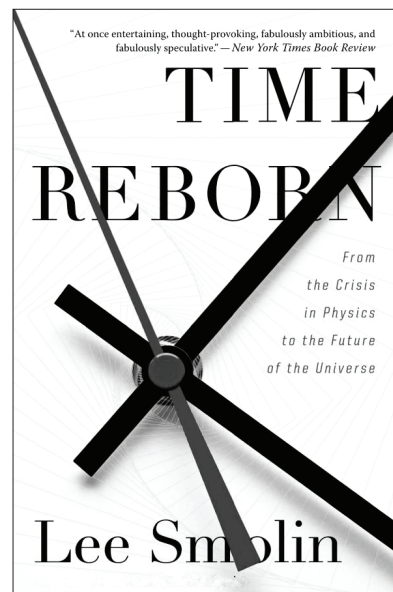
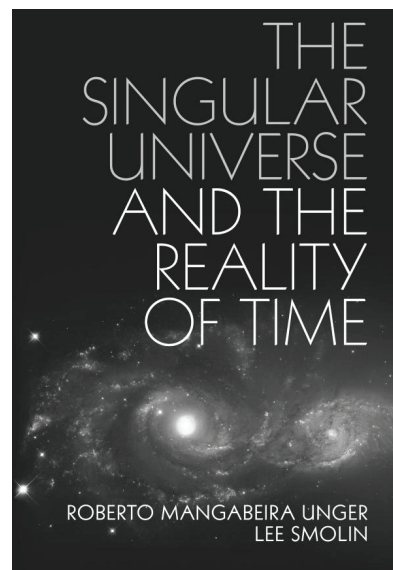
Lee Smolin is a theoretical physicist and Roberto Mangabeira Unger is a philosopher. The message in these two books is essentially the same and the same as that which Smolin has promoted for some time. The books promote a godless and radical departure from the classical way of thinking about the universe, espousing a significant departure from the standard scientific philosophy of the last four centuries.

In *Time Reborn*, Smolin cannot conceive of a universe created by an extant creator who imbued it with immutable laws. His mindset seems to be one that is shocked by the idea that this universe was prepared in a just-right state such that we can exist in it. And this occurs even when he is thinking in evolutionary terms. So to him the idea that the universe occurred just once with initial conditions and laws that allow life to exist is too shocking to contemplate. His answer is evolution. This universe evolved from

a prior universe and its laws evolved along with it.

The main thesis can be summarised as *the universe is singular, time is real and laws change*. By this the authors mean that the universe is all there is, there is no creator, and because we live in a universe that is now in a cooled-down differentiated state (i.e. with galaxies and stars), it must have changed from its initial state (implicitly assuming a hot big bang origin), hence they conclude time is real. This is contrasted with the Newtonian paradigm concept, which has driven science for the past 400 years, where the scientist looks for the timeless description of the whole universe. The believing scientist like Newton would say that he was looking for timeless laws and initial conditions (the creation history), products of the Creator's mind. In those laws there is cause and effect; causation resulting from actual laws, that are themselves unchanging.

Smolin and Unger suggest otherwise; that causation forms a real feature of nature and that it is not just a mental construct but due to real connections in nature. They argue that causation takes place in time and hence implies the reality of time; time would not be real if causal connections simply enacted timeless laws of nature; and these causal connections change in real time. This means the laws of physics evolve. Nothing is immutable, except time itself. Thus they promote *an eternal universe*; a universe that successively evolves through the continuous process of creation and annihilation of the successive universes, wherein the laws of nature evolve. The argument for this evolutionary aspect is novelty. A universe where time is real and laws



evolve allows for novelty—new laws that can change from one universe to the next.

They contrast two cosmologies: one, which includes the Newtonian paradigm, is where laws are immutable and timeless, time is essentially relational, not absolute, as developed in Einstein's Relativity Theory, and there is no novelty, nothing evolves. The second, is where laws are mutable and evolve, time is the only absolute and is real, and novelty arises as part of nature, resulting in new laws. They

argue that “*everything is emergent—everything comes and goes—except time*” itself.

In their choices for the universe they exclude the Creator. The possibility of a transcendent creator who chooses the initial conditions, hence determined the laws upon which the universe is governed, and even intervenes in his creation, is excluded.

In this regard, they write:

“The laws are timeless. They have no history [JGH: meaning, they are immutable, constant]. They underlie and justify causal explanations. *They are, however, themselves without explanation.* To ask why they are is to pose a question that lies in principle beyond the limits of natural science conforming to the Newtonian paradigm [emphasis added].”<sup>1</sup>

This is the crux of the matter. They seek an explanation of this universe without a creator. He, by definition, is excluded from natural science.

So their answer is a universe, or eternal temporal succession of singular universes, wherein the laws evolve, due to a feature of nature itself. In their universes the laws are only partially unchanging; i.e. they slowly evolve, resulting in novelty.

They contrast this with the alternate godless explanation of multiple parallel universes. The promotion of the multiverse results from the need to rescue the Newtonian paradigm. This means that within any one universe in the multiverse the laws are immutable and timeless. Hence, by having an infinite number of universes, we might find ourselves in the one where the initial conditions and laws are such that life could have evolved.

“If, however, these other universes are, as they must be, causally unconnected with our own, and no light-borne information can travel from them to us, this conjecture will amount to no more than a *vain*

*metaphysical fantasy, disguised as science* [emphasis added].”<sup>2</sup>

Their alternative is a succession of universes born from the death of the previous. A universe born from a singularity with infinite density and temperature cannot be comprehended. But universes that do not undergo an infinite density state in a singularity of a big bang can be understood. This is where laws evolve and change but carry some aspect of their past existence into the next.<sup>3</sup> This involves a strong appeal to nature, the pagan concept of Gaia.<sup>4</sup>

The price to pay, they say, for their view of the universe, is that everything is emergent except time itself. There was no beginning. Time had no beginning. The characteristics of the observed universe with its stable structures cannot be the only form of nature. And the view that what is physically real in this universe is what can be described mathematically must be forgone. The sovereignty of mathematics over physics

“... *is intimately related to the assumption of the immutability of the laws of nature and to the invariance of its symmetries, expressed as mathematical equations*”.<sup>5</sup>

The Newtonian paradigm uses mathematics to explain temporal events by timeless laws. They see no such commitment but state that the universe “*is what it is because it was what it was*”.<sup>6</sup>

Their ideas are based on Darwin. According to them, the life sciences have successfully developed an historical science interpretation of the biological evidences, in the rock record etc. Thus they suggest the same for cosmology as a historical science. In so doing they challenge the basis of all operational science, at least on the timescale of the universe. Implicit is the assumption that there is no creator and that the universe evolved to its current state by some characteristic intrinsic to the universe itself. So the singular universe, though from a temporal

sequence of singular universes, and the reality of time—eternal time, “really deep” time—are their answers.

These books attempt to do with the universe what Darwin attempted to do with living things. In this case, the laws of the universe are made mutable, and allowed to evolve from one universe to the next. This speculation is meant to explain the universe we observe, with life evolved in it, without the need for a transcendent creator. In order that we arrive at this state of our current universe all that had to happen was sufficient time. The only absolute in this worldview is the reality of time itself, a lot of time, eternal time. Thus in this worldview time is god.

## References

1. Unger, R.B. and Smolin, L., *The Singular Universe and the Reality of Time*, Cambridge University Press, UK, 2015.
2. Unger and Smolin, ref. 1, p. 21.
3. Hartnett, J.G., On the origin of universes by means of natural selection—or, blinded by big bang blackness, 9 October 2014, [creation.com/on-the-origin-of-universes](http://creation.com/on-the-origin-of-universes).
4. Hartnett, J.G., Development of an ‘old’ universe in science, 30 July 2015, [biblescienceforum.com](http://biblescienceforum.com).
5. Unger and Smolin, ref. 1, p. 44.
6. Unger and Smolin, ref. 1, p. 45.



# A distorted map

## ***Mapping the Origins Debate: Six Models of the Beginning of Everything***

Gerald Rau

IVP Academic, Downers Grove, IL, 2013

Andrew Kulikovsky

Gerald Rau has a Ph.D. in plant breeding from Cornell University and is the founder and chief editor at Professional English International Inc., based at National Chung Cheng University in Taiwan. His professional background and qualifications are in biology, science education, horticulture, plant breeding, and international agriculture, and he has previously taught biology courses at Wheaton College and Trinity Christian College (both in Illinois, USA). Rau has no formal qualifications in history, philosophy, biblical studies, or theology.

According to the author, the book is intended to be

“... a simple map to help high school or college students find their way through hotly disputed territory, to guide their journey from the one-sided and greatly oversimplified arguments they have heard in science textbooks or church sermons to the depth of scientific, theological and philosophical literature that exists” (p. 13).

Rau’s methodology includes objectively presenting and comparing the six basic models used to explain the age-old questions regarding the origins of life, the universe, and everything.

### **Methodology**

In chapter 1, Rau sets out the foundational issue of the whole debate and every related question: the

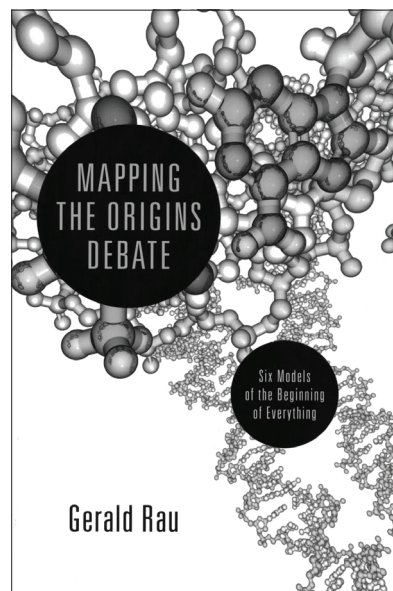
importance of acknowledging the lens through which we select, examine, and interpret the data we employ as evidence in support of our beliefs and in opposition to others’ beliefs.

“... the presuppositions implicit in a person’s philosophy determine the perspective from which he or she views the data, leading to different logical conclusions about which explanation best fits the evidence” (p. 20).

Rau rightly begins from a worldview perspective and acknowledges that a person’s worldview and personal philosophical presuppositions directly affect the way we understand both science and the origins debate in general. He recognises that most people find it difficult to define science because it is applied in many different contexts including theoretical science, experimental science, observational science, and historical science. Rau suggests it involves three components (1) empirical evidence, (2) logical inferences, and (3) necessary presuppositions. He goes on to explain that true objectivity in science is not possible given that individual scientists work from the perspective of one particular theory, which affects what data is collected and how it is interpreted. He adds that

“... objectivity and consensus will be easier to obtain in the experimental sciences than in the historical sciences, particularly those like origins that are closely connected with our philosophical commitments” (p. 26).

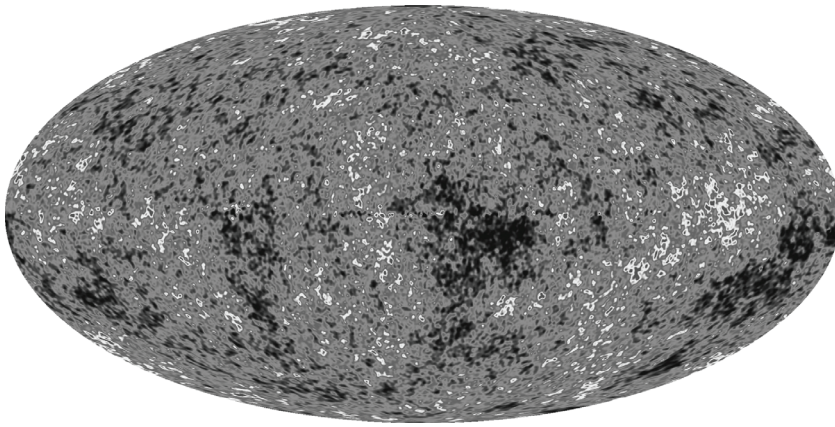
Rau also raises the important question of whether science is the only way of knowing, and in this book he takes the approach that there is “a unity of knowledge—a reality that can be known” (p. 27) although we may use different approaches to procuring that knowledge.



In chapter 2, Rau outlines the six basic models that he wishes to evaluate and compare. They are as follows: naturalistic evolution (NE), non-teleological evolution (NTE), planned evolution (PE), directed evolution (DE), old-earth creationism (OEC), and young-earth creationism (YEC). The chapter also includes a brief discussion of intelligent design and its relationship to the aforementioned models. The points of comparison for his investigation of the competing models of origins include: (1) the origin of the universe, (2) the origin of life, (3) the origin of species, and (4) the origin of human beings. These topics are the subjects of chapters 3–6, which all follow the same format: Rau begins by discussing the relevant evidence or data and then examines how each model interprets this data.

### **Cosmology**

Concerning the origin of the universe, all models accept the standard big bang model except the YEC one. Evidence includes observed redshifts in starlight and Hubble’s Law, the cosmic microwave background radiation (CMBR), the relative abundance of light



**Figure 1.** According to the big-bang model, the CMB is meant to be homogeneous and isotropic, but the observational evidence reveals something quite different.

elements, and fine-tuned universe. Unfortunately, Rau skims over the many problems and discrepancies with all big bang models, although he does highlight the non-observation of dark matter, dark energy, and inflationary period but that's it.

Rau compares how each of the six models interacts with modern cosmology from its beginning at the singularity, the big bang and stellar nucleosynthesis, and on to issues of fine-tuning. He barely discusses inflation, let alone the problems with it. He also makes this spurious claim: "On a large scale, the universe appears remarkably uniform and homogeneous" (p. 71). This uniformity is known as the cosmological principle. However, in a footnote (33), Rau notes that YECs disagree and merely "contend" that galaxies are banded in concentric circles around the original nearby centre, and this gives the appearance of homogeneity, suggesting that this is merely their own eccentric interpretation. Yet, in reality, all the observational evidence goes against the cosmological principle. The universe contains many 'clumpy' areas and 'voids' and the Sloan Digital Sky Survey (SDSS) indicates that galaxies are distributed in concentric shells around our own galaxy, and the shells of galaxies appear to be more dense closer in and less dense further out.<sup>1</sup>

In addition, the Wilkinson Microwave Anisotropy Probe (WMAP) data produced detailed maps of the cosmic microwave background radiation but rather than showing an isotropic universe, they revealed a cosmic north and south pole and a cosmic equator!<sup>2</sup>

When dealing with the YEC approach to cosmology, Rau presents a superficial description of Russ Humphreys' 'white hole' cosmology which includes time dilation as well as the possibility of a Euclidean (timeless) zone.<sup>3</sup> Moreover, no references to other contributors to YEC cosmology (e.g. John Hartnett or Jason Lisle) can be found.

### Evolutionary theory

Regarding the origin of life, the things that require an explanation include the initial appearance of life from non-life, the encoding and transmission of genetic information, and the apparently irreducible complexity of living things.

On the origin of species, the data in question includes the dating and sorting of fossils—both vertically and geographically—and their apparent 'progression' from simpler to more complex. Rau acknowledges the lack of transitional forms and the appearance of what seem to be explosions of rapid speciation as well as evidence of mass extinctions.

Other data covered includes genetic complexity, selection and mutation, population genetics, and homeotic genes, as well as genetic similarities and symbiosis.

Rau rightly points out that the term 'evolution' has been defined and used in different ways: (1) change over time, (2) change in frequency of alleles in a population, (3) common descent, (4) speciation, (5) origin of higher order taxa, (6) origin of all living organisms by undirected natural processes, and (7) the neo-Darwinian synthesis. Proponents of evolution often employ a bait-and-switch technique by first utilising definitions (1) and (2) to demonstrate that evolution has been observed, and then, after switching to the other definitions, asserting that biological evolution is an observed fact.

With respect to the origin of human beings, the major evidence consists of 'hominid' fossils and similarities between human beings and chimpanzees. Rau highlights the relative sparsity of human-like fossils. There are less than 100 significant fossils that are dated at more than 200,000 years (according to the evolutionary timescale) and most are merely partial skulls. Only four have significant skeletal remains. In addition, there are about 50 skeletons of Neandertals or modern humans. Again, the author goes on to explain how the different views interpret the above data, but his treatment of the YEC interpretation is extremely superficial. This is a serious oversight because the YEC interpretation is quite different to the others. Moreover, he does not cite or reference (even in the bibliography) any of Marvin Lubenow's extensive work on this very subject.<sup>4</sup>

There is a strong passive-aggressive attitude toward the YEC view throughout the book. Regarding scriptural interpretation, he presents these snide and hyperbolic comments:

“Many advocates of YEC are totally convinced that their interpretation of Scripture is correct, and they therefore call all others compromisers, deceived by the lies of Satan, who substitute the changing ideas of science for the eternal, unchanging truth of the Bible” (p. 148).

None of these comments are supported with actual references to YEC writers. While YECs are no doubt convinced of their interpretation of Scripture, so are all those who disagree with them! He continues:

“At the same time theistic evolution proponents representing various models claim it is YEC that is violating hermeneutical principles by forcing on Scripture a scientific interpretation that was never intended, and they criticize creation advocates for ignoring what they consider to be the plain facts of science, thus placing a stumbling block in the way of scientists who might otherwise be more open to Christianity” (p. 149).

Again, no substantiation is provided. In reality, the opposite is the case: YEC writers have repeatedly highlighted the hermeneutical gymnastics and exegetical fallacies employed by those who reject the traditional interpretation of creation in six literal days.<sup>5</sup>

In addition, Rau—like many other YEC critics—misrepresents the YEC hermeneutical method as ‘literalism’ and then goes on to highlight the many places in Scripture that YECs

do not adopt a literal interpretation. But this a straw man argument. Interpreting the days of creation as literal 24-hour days does not mean that one must adopt a literalistic hermeneutic. YECs routinely employ the standard historical-grammatical exegetical method, and it is the judicial application of this method that leads us to interpret the creation days as normal literal days.

### Distorted presentations

Chapter 7 is titled “What we can learn from each”. In it, Rau attempts to summarise the positive evidence that has been marshalled in support of each view that cannot be dismissed by the other views. In support of naturalistic evolution, Rau cites the whale evolutionary sequence and big bang cosmology. However, with respect to whale evolution, none of the so-called ‘transitional forms’ (*Pakicetus*, *Amubulocetus* and *Rodhocetus*) stand up to scrutiny. Rather, they reveal a pattern of extremely wishful and imaginative thinking, if not outright fraud.<sup>6</sup> For example, *Pakicetus* was presented on the cover of *Science* in 1983 as a whale-like creature when only an incomplete skull had been found. When the rest of *Pakicetus* was found in 2001, it was nothing like a whale!

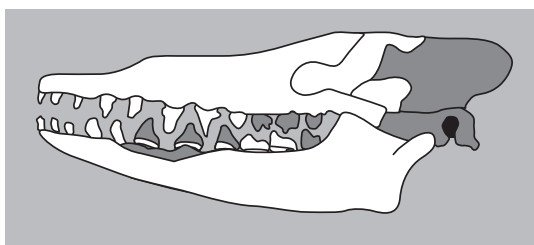
Similarly, regarding the evidence for big bang cosmology, Rau gives the impression that the theory has made a string of accurate and detailed predictions including the existence and temperature of the cosmic microwave background radiation (CMBR). Yet, he fails to mention that numerous other scientists also predicted the existence of, and indeed a more accurate temperature for, the CMBR without reference to big bang cosmology.<sup>7</sup> He also fails to mention the

numerous other direct observations that big bang cosmology cannot explain including quantised redshifts, disparate redshifts of physically connected stellar objects, the clumpy distribution of the observed universe, the existence of cosmic poles and a cosmic equator (discussed above) and the failure to detect dark matter despite it supposedly being the predominant ingredient of the universe.

Rau also provides a brief discussion of the contributions of YEC scientists to the scientific debate. He begins by pointing out that they have been instrumental in highlighting flaws in the other views and in bringing to light evidence that is well-known in the scientific community but has been slow to find its way into textbooks and the popular press. In addition, Rau acknowledges that YECs have proposed their own scientific models in cosmology, plate tectonics, the Ice Age, and catastrophic events such as the eruption at Mount St Helens, although he adds that this work has largely been ignored by the mainstream scientific community. Rau states that “[i]n recent years” (p. 161) YEC scientists have established their own peer-reviewed scientific journals and the accompanying footnote (9) cites *Answers Research Journal* published by Answers in Genesis in the USA. Given that the *Creation Research Society Quarterly* has been published by the Creation Research Society continuously since 1964, and the *Journal of Creation* (formerly *Creation Ex Nihilo Technical Journal* and then *TJ: The In-depth Journal of Creation*) has been published by Creation Ministries International continuously since 1984, one has to wonder at the quality and depth of Rau’s research—especially with respect to the YEC view.

### Philosophy and epistemology

Rau is quite right to point out that—when discussing the origin of life—YECs (and OECs) have to



**Figure 2.** *Pakicetus* was presented in the media as a whale-like creature when only an incomplete skull had been found. But when the rest of *Pakicetus* was found years later, it was nothing like a whale!



admit that they have no scientific explanation or mechanism, and nor do they need one because, as Genesis 1 teaches, the origin of life was an explicit supernatural act of God Himself. Moreover, Rau notes that the evolutionary models are no better off because they too have no viable scientific explanation. ‘God did it’ and ‘nature did it’ are both religious explanations! He also shows a healthy scepticism regarding scientific objectivity:

“Science is not the totally objective, dispassionate search for truth that some believe it to be ... . Much good research is not funded because it does not meet [specific] criteria, and researchers who present results at odds with the viewpoint of the funding institution are not likely to get funded again” (p. 173).

Rau points out that each position is ultimately based on “different philosophical presuppositions that are outside the realm of science” (p. 176). According to Rau, the key presupposition is the definition of science itself. He appears to think that it is possible to define science in a way that allows the possibility of the existence of, and interaction with, a supernatural realm. However, in my view, the problem is not the definition of science but the constraints imposed by naturalism and materialism. Science, by definition, excludes the supernatural. But why should we limit the acquisition of knowledge to scientific enquiry? This *a priori* excludes—with no scientific basis—any possibility of the supernatural realm and any possibility of supernatural revelation. In other words, naturalistic and materialistic epistemological presuppositions automatically exclude any evidence or inferences that point to an Intelligent Designer as the Creator of the universe and all life within it. This approach illegitimately precludes all other views except naturalistic evolution. Nevertheless, Rau is mostly right in claiming that “[t]here is a war going

on, but it is not a war between science and religion. Rather, it is a war about what science is, a war that is philosophical more than religious” (p. 189). I would say that the war is actually about knowledge and how it may be acquired, i.e. the branch of philosophy called epistemology. It is also religious in the sense that all positions have faith in their own epistemological assumptions and presuppositions.

### Conclusion

Rau matter-of-factly recites many of the claims and arguments made by proponents of the various views, and one gets the impression that he presupposes the truth and legitimacy of the science behind all these claims. Moreover, he only occasionally provides actual references to specific published works. This makes it very difficult to check on the veracity and accuracy of his presentation of each view.

Rau’s goal in *Mapping the Origins Debate* is to guide students through the competing claims of each position and to introduce them to “the depth of scientific, theological and philosophical literature that exists” (p. 13). Unfortunately, Rau has only partly achieved this goal. On the positive side, the book has an appendix containing extensive charts that tabulate the differences between all six views for easy comparison. A second appendix attempts to summarise each view’s interpretation of the Genesis account. This summary is so brief (amounting to only two pages) that it is practically useless.

Again, Rau’s lack of direct citation and reference to original works give me the impression that we are simply getting Rau’s very limited understanding of the different views and their interpretation of the data. Indeed, the bibliography—consisting of a mere nine pages—is completely inadequate for a work that covers so much ground.

In addition, there is a fatal flaw in Rau’s methodology. Although he acknowledges the inherent limitation of assuming a naturalistic and materialistic epistemology, his choice of things to compare are all material elements! This loads the debate in favour of the evolutionary views that adopt naturalistic and materialistic mechanisms. But what about non-material phenomena such as language, emotion, morality, and the notion of thought itself?

Rau does not provide any analysis or conclusion regarding which view is best or which has greater claims to truth and validity, but his presuppositions reveal his preferred position. One thing is certain: he is no advocate or proponent of the young-earth creationist’s view.

### References

1. Hartnett, J., New evidence: we really are at the centre of the universe, *J. Creation* 18(1):9, 2004.
2. Williams, A. and Hartnett, J., *Dismantling the Big Bang*, Master Books, Green Forest, AR, pp. 135–136, 2005.
3. Rau appears to have got his information from a brief summary article published in the Institute of Creation Research newsletter *Acts & Facts* rather than Humphreys’ book *Starlight and Time* or his *J. Creation* articles.
4. See especially Lubenow, M.L., *Bones of Contention*, Baker Books, Grand Rapids, MI, 2004.
5. Kulikovskiy, A.S., *Creation, Fall, Restoration: A Biblical Theology of Creation*, Mentor, Fearn, Ross-shire, UK, 2009.
6. See Batten, D., Whale evolution fraud, *Creation* 36(4):34–35, 2014; [creation.com/whale-evolution-fraud](http://creation.com/whale-evolution-fraud).
7. Assis, A. K.T. and Neves, M.C.D., History of the 2.7K Temperature Prior to Penzias and Wilson, *APEIRON* 2(3):79–87, 1995.

# Death-camp doctors— Darwin's proctors

***Giants: The Dwarfs of Auschwitz***

**Eilat Negev and Yehuda Koren**

MJF Books, New York, 2013

*Jerry Bergman*

This book about a dwarf family focuses on the infamous medical research done by the Nazi doctors and how and why the research was done. A major reason for the research was an attempt to apply Darwinism to science with the goal of producing a superior race.

During the 1930s and 1940s, the Lilliput Troupe family of singers dazzled audiences with their unique vaudeville performances. The only all-dwarf show then, their small stature earned them fame—and, ironically, ultimately saved their lives in Auschwitz. After descending from the cattle train in the Auschwitz death camp, the Ovitz family—seven of whom were dwarfs—was plunged into the Nazi horrors during the darkest moment of modern history. They were separated from the other victims on the orders of Dr Joseph Mengele (1911–1979). Formerly “showered with flowers and besieged for autographs, these entertainers ... were now declared a ... genetic error that the state set out systematically to erase” (p. 91).

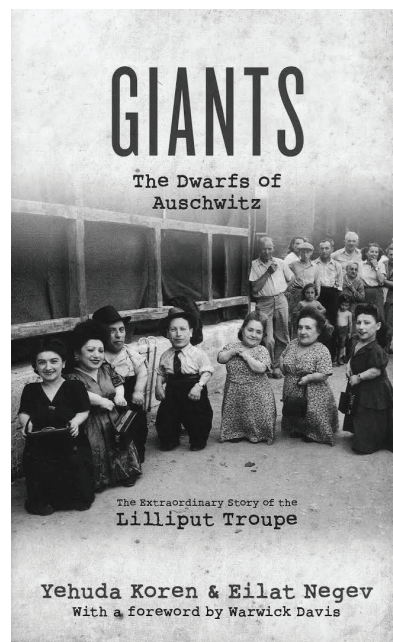
## Enter Mengele

In 1930 Mengele enrolled as a medical student at the University of Munich. He soon became intrigued by the then burgeoning field of Darwinism, heredity, and eugenics.

In 1935, Mengele received a Ph.D. in anthropology for a thesis “attempting to demonstrate that one could differentiate racial groups according to jaw shape” (p. 70). He claimed that “dental irregularities were hereditary and tended to appear with other hereditary abnormalities, like idiocy and dwarfism” (p. 71). Mengele’s doctoral advisor, Professor Theodor Mollison (1874–1952), even boasted that he could tell a Jew merely by looking at his photograph. A year later the 25-year-old Mengele was licensed to practice medicine. In 1937 he joined the Nazi Party, and the next year he joined the SS.

Mengele’s work was highly influenced by the Darwinian scientific establishment. Throughout his life, “Mengele instinctively bowed to authority figures; a charismatic science teacher shifted his interest from the arts to the natural sciences” and an esteemed professor turned his interest to Darwinism (p. 70). The latter’s Ph.D. work was the inspiration for Mengele’s genetic research in Auschwitz (p. 37).

After two years of military service, Mengele was wounded and reassigned to the Berlin headquarters of the Race and Settlement Office, which was responsible for the concentration camp medical experiments. Mengele was then able to resume his close relationship with his patron, Professor Otmar Freiherr Verschuer, who had recently moved “to Berlin to take up his new post as the director of the Kaiser Wilhelm Institute of Anthropology, Human Heredity, and Eugenics” (p. 72). Verschuer was a “renowned geneticist and ardent admirer of Hitler” (pp. 70–71). Mengele’s doctoral advisor’s



“... enthusiastic letter of recommendation won Mengele a highly coveted position as a research assistant at the Institute for Hereditary Biology and Racial Purity at the University of Frankfurt ... ‘Mengele was now at the epicenter of Nazi philosophical and scientific thinking, which held that it was possible to select, engineer, refine and ultimately purify the race’” (pp. 70–71).

The authors describe Dr Mengele as obsessed with eugenics. He ordered a series of loathsome experiments on the Ovitz family, and concurrently developed a disturbing fondness for his “human lab-rats”. Mengele “did not want simply to succeed”, but to become so famous that “his name would be in encyclopedias” (p. 70). He succeeded, but not for the reason he had envisioned.

Due to the war, Verschuer’s research on twins suffered a major setback because his access to new research cases dried up. Verschuer therefore encouraged Mengele to “apply for a position at Auschwitz, where they would have continual access to an unlimited supply of human specimens”. Mengele was



**Figure 1.** Auschwitz I concentration camp entrance

accepted, and on 30 May the 32-year-old doctor arrived at the Birkenau-Auschwitz complex. Because Auschwitz was eventually no longer able to deal with “the mass of racially undesirable peoples” sent there, the Birkenau camp began operation in February of 1942 (p. 72).

Mengele was then appointed chief physician of the Gypsy camp section, responsible for selecting which of the new camp arrivals should be sent to their immediate death or be assigned to the slave labour section of the camp. Soon his “enthusiasm, ambition, charisma and cruelty set him apart from the other death-camp doctors” (p. 72).

The ambitious Mengele was soon no longer content to work as Verschuer’s assistant, as he had up to this point, but wanted his own research project to better understand race and Darwinism; and in the spring of 1944, as Birkenau was preparing for a massive influx of Hungarian Jews, Mengele saw his opportunity. During “... his first year in the camp, he had mainly experimented on a few dozen cases, most of them sets

of twins, that he had discovered among the Gypsies and Czech Jews ... . But now, with the imminent arrival of hundreds of thousands of Jews, research vistas of unlimited scope and variety were about to open up for him” (p. 88).

After the mass extermination of almost half a million Hungarian Jews, the camp authorities turned to the Gypsies. The Nazis had “been undecided in its policies towards them: should they be exterminated as an inferior race, ... [or] locked away and sterilized?” (p. 119). The decision was they should be exterminated as an inferior race, so in May of 1944 the SS surrounded the Gypsy camp

“... in an attempt to lead all 6,000 inmates to the gas chambers. The troopers, however, met with fierce opposition—men and women armed with knives, iron pipes and any metal object, dull or sharp, that they could find ... . As a result, the camp administration changed its plan. Able-bodied Gypsy women were sent to slave labor camps, and Gypsy men from Germany were sent to the Wehrmacht to serve as live mine detectors” (p. 119).

Mengele once confided to the distinguished Jewish pediatrician Berthold Epstein (1897–1962), who was then imprisoned at the camp, that his (Mengele’s) goal in the war was to use his achievements “as a springboard towards a professorship ... in the shape of a scientific treatise that would confirm ... the indispensability of his research”.

“‘We are enemies—you will not get out of here,’ Mengele bluntly told Epstein. ‘If you perform scientific work for me and I publish it in my name, you will prolong your own life.’ As a result, Epstein extensively researched a deadly gangrene of the face and the mouth, conducting tests on Gypsy children and adolescents” (p. 88).

Epstein did get out of Auschwitz alive, although the rest of his family did not.

An inmate artist named Dina was assigned to draw other inmates. Not happy with her apparent preference for good-looking Gypsies, Mengele himself selected “elderly women and men ... to acquire visual documentation to support his racial theory” and to illustrate a book that he was writing (p. 100). Also, “a female Polish prisoner took the hand and fingerprints of all the inmates selected by Mengele for his experiments. Mengele instructed Dina to sketch their skulls, ears, noses, mouths, hands and feet” for his book (p. 100).

### The end of the Nazi Darwinian eugenics program begins

During his year as the head physician of the Gypsy camp, Mengele developed cordial relationships with many of its inmates. He had special

“... fondness for the twin children and often smiled when they called him ‘Uncle Mengele’. But when he received the final order to liquidate the remaining 2,897 Gypsies, most of them women and children, he carried it out obediently and diligently. ... he now made use of their blind trust by enticing boys and girls out of the hiding places with the same candies he had offered them after painful experiments. As he led them to their death, he ignored their frantic pleas” (p. 120).

After the annihilation of the Gypsies, Mengele was appointed First Physician of the Auschwitz-Birkenau camp. In this position he continued to direct a myriad of medical tests on his new 350 Jewish victims, 250 of them twins (p. 123).

Because his former mentor, Prof. Verschuer, stressed that heredity can be most effectively researched on





**Figure 2.** The main entrance to Auschwitz II (Birkenau) concentration/extermination camp

complete families, when Mengele learned

“... that a large family with dwarf traits had just arrived he did not waste a moment. ... Crowding around him, the Ovitzes did not waste their chance to dazzle him. They answered his questions eagerly, and Mengele was indeed dazzled: ‘I now have work for twenty years,’ he said joyfully” (p. 74).

The first time the Lilliputs were evaluated at the camp clinic, the doctors that examined them assumed this “... was a routine admission procedure. But when the examinations were repeated day after day, it soon dawned on them that they had been selected for some medical purpose. Josef Mengele was only one of dozens of doctors who performed criminal experiments on the inmates of Auschwitz-Birkenau. Whereas German law protected laboratory animals, there were no limitations whatsoever on what could be done to human guinea pigs in the death camps” (p. 74).

Furthermore, the working conditions at the camp were ideal.

The laboratories were well equipped, and “the cream of academia was present—people with an international reputation,” allowing him to “carry out experiments on human beings usually only possible on rabbits” (p. 86). Dr Mengele “felt no compunction about experiments conducted upon the Jews. He argued that since they were all doomed to die anyway ... it would be a waste for science not to use them” for his brutal research to better understand evolution (p. 86).

#### **Science used to research Darwinian based racism**

The research was completed by a team of medical specialists who exploited the “unlimited pool of subjects to test any new substance or procedure that captured their eugenic interest, such as efficient, cheap methods of implementing mass sterilization and eliminating the mentally, genetically or racially unfit” races (p. 87). In the end, “thousands of young prisoners suffered radiation, repeated injections with various chemical substances, and operations without anesthetics. Those who did not die in the name of German science

often ended up gruesomely maimed” (p. 87). When a doctoral student, Mengele published an article that argued

“... it is not useful to take as many measurements as possible: one must restrict oneself to the most significant ones.’ However, with the unlimited time, human resources and research possibilities available at Auschwitz-Birkenau, Mengele ... unleashed himself and his team on his subjects in a relentless quest for detail” (p. 105).

After inmate anthropologist Dr Martina Puzyna had completed the initial round of anthropometric measurements, the subjects were examined by a team of prisoner

“... specialists: an internist, a neurologist, a psychiatrist, an ophthalmologist, a dermatologist, a surgeon, a urologist, and an ear, nose and throat man—all of them prisoners ... . While Mengele reviewed all the results, he himself conducted none of the actual examinations” (p. 107).

The specialists “... evaluated the dwarfs’ entire anatomy by comparing the physical features and psychological

characteristics to those of average-sized humans in search of irregularities that would account for their arrested growth. ... the ... dwarfs supplied samples of urine, stool and saliva that were analyzed” (p. 107).

Dr Puzyna, although “ambivalent in her judgment of Mengele’s work ... insisted long after the war that its results ‘were of immense value to the science of anthropology’” (p. 105). The Ovitiz family

“... felt they were consistently being violated for apparently needless and endless samplings, puncturings and probings. They saw their medical files grow steadily thicker, document by document, yet they could see no medically constructive or beneficial purpose whatsoever behind it all” (p. 123).

The research goals included deciphering genetic differences of Jews, Gypsies and others to determine their resistance, or lack thereof, “to various infectious diseases, and assemble as much material as possible from genetically affected twins or families” (p. 87). The scientists felt the key to race was in the blood. As a result, in

“... the 1940s, medicine was obsessed with blood and its constituents. It was generally believed that blood plasma retained all traces of illness and contained all genetic traits. German scientists considered blood as a key to the differentiation between superior and inferior races” (p. 93).

This is why “Mengele’s research relied primarily on blood tests, X-rays and anthropometric measurements. He had neither the time nor the inclination to test his hundreds of victims personally but then, he did not need to—not with the abundance of expert professionals among the hundreds of thousands of people

passing through the gates of Auschwitz-Birkenau” (p. 103).

### **The focus on the eugenic racist ‘blood’ claims**

Although Mengele acted according to standard practice, “he had no idea what he was looking for”. For this reason, the repeated tests took large amounts of blood for his research for no apparent reason (p. 103). Some gave blood to test for syphilis, even in the children, including baby Shimshon. “They, as well as the adults, all proved negative” (pp. 96–97).

“The Ovitizes were never told which tests were going to be performed on them on any particular day, but ... would find themselves lying naked and face down on the examination tables, and the bustle of medical activity around them only intensified their anxiety as they wondered where precisely their bodies would be pierced or jabbed or poked, and to what violent and devastating effect” (p. 123).

After the camp’s liberation, “in laboratory report-forms on samples of blood, saliva, urine and faeces, several thousand lab results were found intact” (p. 91).

When the Russian army liberated Auschwitz, the entire Ovitiz family was still alive. After the war, Mengele “followed the Nuremberg trial of his former Nazi medical friends and colleagues in December 1946 with some degree of apprehension”. Seven were hanged; five received life sentences. “On the other hand, the ... [rapid] social and professional rehabilitation of his superiors, ... [and] their embrace by [the] post-war Germany ... academic community—must have stirred in him considerable envy” (p. 209).

For example, Mengele’s professional sponsor, Verschuer, the “head of the genetic and hereditary research program ... was declared a Nazi

sympathizer ... was fined [only] 600 marks”. Then, in “1951, he became Professor of Human Genetics at the University of Münster; three years later, he was promoted to the position of dean of the medical faculty ... honours were bestowed on him by the American, Italian, Austrian and Japanese societies for [his work in] human genetics” (p. 209).

Another example is Mengele’s academic competitor, Professor Hans Grebe, who soon obtained an academic “position in the department of human genetics at the University of Marburg” and in 1957 became president of the German Association of Sport Doctors. Ironically, the medical records kept by

“... Verschuer at the Kaiser Wilhelm Institute are not available to researchers: in a bizarre irony, many decades after they were murdered, the Nazi doctors’ Jewish victims have been transformed by German officials into esteemed patients whose right to privacy must be steadfastly safeguarded” (pp. 209–210).

In an effort to dissociate it from its Nazi past, in 1948 the Kaiser Wilhelm Institute was renamed “the Max Planck Institute”. In June 2001, the society’s president, Professor Hubert Markl, admitted that scientific evidence exists “proving beyond the shadow of a doubt that directors and employees at the Kaiser Wilhelm Institute were together intellectually responsible for, and sometimes even actively collaborated in, the crimes of the Nazi regime” (p. 210). The fact is “The biggest crime in history was carried out under the direction of leading scientists and distinguished institutions” who were under the spell of Darwinian eugenics (p. 210).

# Another devastating critique of neo-Darwinism

***Evolution: Still a Theory in Crisis***

Michael Denton

Discovery Institute Press, Seattle, WA, 2016

Dominic Statham

Michael Denton is a Senior Fellow at the Discovery Institute's Center for Science and Culture. He read medicine at Bristol University in the UK and subsequently gained a Ph.D. in biochemistry from King's College in London. In 1985 he published *Evolution: A Theory in Crisis*<sup>1</sup> in which he demonstrated that the living world is fundamentally discontinuous and shows no evidence of the functional continuum predicted by Darwinian theory. The major taxa-defining characteristics, such as mammalian hair or avian feathers, he argued, are not led up to via a series of functional intermediates, and this undermines Darwinian adaptive gradualism at its heart.

Denton is a 'typologist', holding that there are deep, unbridged divisions in the order of nature. As argued by eminent biologist D'Arcy Wentworth Thompson, "Nature proceeds from one type to another ... and to seek for stepping-stones across the gaps between is to seek in vain, for ever" (p. 12). Similarly, Denton rejects as wholly unsupportable the Darwinian mantra, "*Natura non facit saltum*" (Nature does not make leaps).

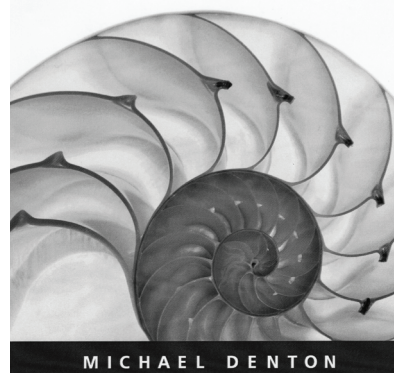
His new book, *Evolution: Still a Theory in Crisis*, provides much additional material and demonstrates, with even greater clarity, how the natural world is characterised by discontinuity and what he describes as 'taxon-defining homologs'—

unique biological traits shared only by members of a particular group. Examples include the enucleated red blood cell and placenta found only in mammals, the insect body plan, the pentadactyl limb shared by all tetrapods, and the amniotic membrane found only in reptiles, birds and mammals. As Denton makes clear, these 'types' are undeniably real and isolate one group from another. They are not, and could not have been, led up to via a series of intermediates, and their distinctiveness actually provides the basis for classification.

Despite his rejection of neo-Darwinism, Denton is still a 'molecules to man' evolutionist (p. 116), and subscribes to 'descent with modification' as the explanation for homology (pp. 111, 112). He is, however, an advocate of 'structuralism' rather than 'functionalism', believing that, primarily, biological order has arisen from the self-organising properties of biomatter, rather than from adaptation. The latter, he claims, played only a minor role in determining the forms of plants and animals. Hence, he understands major evolutionary novelties and the taxon-defining homologs to have originated *per saltum*, i.e. in leaps without any intervening stages. In his thinking, these would not have arisen from random macromutations, producing something akin to Goldschmidt's 'hopeful monsters',<sup>2</sup> but would have been directed by natural laws. According to Denton:

"Just as a crystal of common salt arises when a solution of sodium chloride ions evaporates, a snow crystal forms when water freezes, or a new atom arises when two nuclei collide and fuse in a stellar interior, so the basic homologs

## EVOLUTION: STILL A THEORY IN CRISIS



or Types (the 'atoms' of biology) should arise, from the cellular to the organismic level, from the self-organising properties of particular classes of matter" (p. 251).

These paths of evolution, he believes, are "part of nature's deep causal structure, prefigured into the order of things from the beginning" (p. 116).

Unsurprisingly, very little of the book is devoted to justifying this claim, and the details of these hypothetical processes are conspicuous by their absence. Whereas the laws by which salt and ice crystals form are observable in the laboratory, there is no evidence that matter contains the information needed to reorganise the genome and generate novel complex biological structures—either in small steps or in leaps. Moreover, it would seem remarkable that natural processes capable of originating something as complex as the human brain could have escaped the notice of researchers for so long.

Denton, of course, is not alone in advocating self-organisation as the means by which evolution could have progressed, and supporters of this idea include a growing number of leading



biologists.<sup>3</sup> However, although they have no doubts about the inadequacy of Darwinian explanations, they are clearly unable to present a scientific case for such an alternative. One of their number, cognitive scientist Professor Jerry Fodor, for example, confessed, “I don’t think anybody knows how evolution works.”<sup>4</sup>

Despite Denton’s naturalistic worldview, *Evolution: Still a Theory in Crisis* contains much information useful for creationists, particularly as it is clearly written and largely accessible to the non-specialist. Drawing from a wide range of biological disciplines, he demonstrates, beyond all reasonable doubt, the scientific bankruptcy of neo-Darwinism.

### Non-adaptive order

Denton argues that a great deal of biological order has never been shown to be adaptive, in either extant or ancient forms, and therefore “the whole of the Darwinian edifice stands on sand” (pp. 75–76). What selective advantage is found in the concentric whorls of flowers? Why do nearly all mammals have seven neck vertebrae (including the giraffe)? Why do *Longicornia*<sup>5</sup> beetles have eleven joints in their antennae? Darwin’s explanation—that such homologs once functioned in an unknown ancestral form—Denton regards as no more than a weak “*ad hoc* legitimation” (p. 74). Descent with modification, he says, can explain *why* all members of a clade<sup>6</sup> share a homolog, but it cannot provide a causal explanation for *how* the homolog originated.

Another interesting example is the bones in the skull of the human foetus. These have gaps (fontanelles) which enable the head to compress as it passes through the birth canal. However, the same construction is found in the head of the kangaroo embryo, which is born as a tiny joey, and also in birds which hatch from an egg (p. 66). What function did this

serve in the putative common ancestor of mammals and birds? Even the great icon of evolution, the pentadactyl limb, Denton argues, has no adequate Darwinian explanation. Just as a fashion designer’s initial concept has to be tailored to an individual, so the pentadactyl limb is not adaptive in itself and must first be tailored to facilitate a particular function—as the arm of a man or the wing of a bat or the leg of a horse (p. 65).

He also asks how neo-Darwinism can explain why/how such a limb design changed from being evolvable to immutable: “If the homolog was ‘fluid’ during the transition, why and how did it become fixed when the pentadactyl pattern finally emerged?” (p. 79). In a later chapter he observes: “It is surely the ‘best kept of all evolutionary secrets’ that the inference to descent with modification depends on the fixity of the Type—or more properly, the invariance of the taxa-defining homologs ... . How ironic that for Richard Dawkins and other defenders of the Darwinian faith the very notion of *evolution* depends on the fixity of the Type [emphasis in original]” (pp. 106–107).

### The fossil record

Denton quotes Stephen Jay Gould:<sup>7</sup> “Can we invent a reasonable sequence of intermediate forms—that is, viable, functional organisms—between ancestors and descendants in major structural transitions? ... I submit, although it may only reflect my lack of imagination, that the answer is no” (p. 107).

While Denton would agree that the fossil record supports the view that tetrapods evolved from lobe-finned fish, he accepts that the rocks do not contain transitional forms. The explanation, he says, is that intermediate species never existed and the new structures arose suddenly. This, he argues, is true of

evolutionary novelties generally—a view also held by a number of leading researchers such as Professor Gareth Nelson (formerly curator of vertebrate zoology at the American Museum of Natural History), geneticist and philosopher of science Professor Massimo Pigliucci, and evolutionary biologist Professor Günter Wagner (p. 109). Denton opines that the fossil record is consistent with fish evolving into people, but is emphatic that “there are *no transitional forms leading to the actualization of each novelty* [emphasis in original]” (p. 109).

### The enucleate red blood cell

One taxa-defining homolog, characteristic of all mammals, is the enucleate red blood cell, on which Denton writes with considerable authority, this having been the subject of his Ph.D. thesis. Most organisms retain the nucleus in their red blood cells, but mammals are an exception. Towards the end of its development, the mammalian red blood cell ejects this, resulting in an enucleate cell. Denton writes:

“Cells cannot have a nucleus ‘half-in’ and ‘half-out’ of the cell. The intermediate position is not only unknown in the whole domain of nature, but is self-evidently unstable ... . So here is one of the defining traits of the class Mammalia that is definitely *not* led up by any known functional continuum ... . In addition, the process is extremely complex ... [and] it is clear that much of the cell’s basic cytological machinery is co-opted in absolutely unique ways to ‘push’ the nucleus to the side and eventually out of the cell ... . Between a nucleate and an enucleate cell is a quantum jump ... a process involving a host of biochemical and cytological mechanisms, which necessitates re-engineering the entire cyto-architecture of the cell to that end

[emphasis in original]” (pp. 130–136).

One must also wonder why mammals bothered to evolve an enucleate erythrocyte, since reptiles and birds manage fine with red blood cells that keep their nuclei.

### Endometrial stromal cells

The endometrium is the inner membrane of the mammalian uterus. During the menstrual cycle, this grows to a thick, blood-vessel-rich glandular tissue layer into which a fertilised egg can be implanted. An essential step in this process involves the conversion of what are called ‘stromal fibroblast cells’ into ‘endometrial stromal cells’ (ESC), which are unique to placental mammals. This transformation is extremely complex and requires extensive reprogramming of many cellular functions. Denton comments, “[I]t is hard to believe that the various proteins and other biochemicals synthesized in the ESC ... could have been of any adaptive utility individually in preparing the uterus for implantation” (p. 138). He continues:

“In an attempt to elucidate the likely complexity of the new gene circuits and novel gene expression patterns associated with the origin of a novel cell type they [Günter Wagner’s group at Yale University] documented the genetic changes associated with the evolution of the ESC. They ‘found that 1,532 genes were recruited into the endometrial expression in placental mammals, indicating that the evolution of pregnancy was associated with a large-scale [unique] rewiring of the gene regulatory network’” (p. 139).

Unsurprisingly, Professor Wagner concluded, “It is questionable whether the origin of complex novelties—such as the origin of new cell types, which involves the recruitment of hundreds of genes—can be achieved by ... small-scale changes” (p. 140). The idea of Denton and others that new cell types

could evolve *per saltum*, however, is surely even more absurd.

### Orphan genes

‘Orphan genes’ (also referred to as ‘ORFans’) have no homologs in other lineages and, in evolutionary thinking, must have originated *de novo* from non-coding sequences, rather than as modified forms of existing genes. Recent research indicates that these are found in all genomes and make up a significant proportion of protein-coding genes—perhaps up to 30% (p. 143).

To evolve a protein-coding sequence from a non-coding sequence, however, is not all straightforward. For example, a gene requires an open reading frame (i.e. a stretch of DNA without any ‘stop codons’), a promoter capable of initiating transcription and a sequence that encodes a protein serving some useful purpose. It must also be present in a region of the open chromatin structure that permits transcription. Professor Adam Siepel asks, “How could all of these pieces fall into place through the random processes of mutation, recombination and neutral drift—or at least enough of these pieces to produce a proto-gene that was sufficiently useful for selection to take hold?” (p. 142). Denton comments:

“That new protein-coding genes can originate *de novo* is certainly one of the most ‘unexpected tales’ of the new era of genomics ... The terms used by researchers in the field—terms such as ‘enigmatic’, ‘mystery’, ‘unclear’ and other such expressions of amazement—capture something of the challenge the ORFans are seen to pose to traditional gradualistic notions of gene evolution” (p. 144).

Moreover, in an evolutionary scenario, after a new gene has arisen, it would be necessary for an associated gene-control system to evolve. However, as pointed out by Denton,

“the mere ‘turning on’ of a gene is accompanied by a vast complex of regulatory mechanisms to ensure the expression of the gene in the right place at the right time and in the right amount. Such controls are obligatory to avoid molecular chaos in the cell” (p. 226).

### More on the pentadactyl limb

The ‘autopod’ is the hand/wrist in the forelimb and foot/ankle in the hindlimb. In evolutionary thinking, the same patterns are found in amphibians and amniotes because the basic structure was inherited from the fish fin. Denton, however, quotes recent researchers<sup>8</sup> who make the following remarkable admission:

“... although fish have the Hox regulatory toolkit to produce digits, this potential is not realised as it is in tetrapods, and as a result we propose that fin radials—the bony elements of fins—are not homologous to tetrapod digits” (p. 160).

Günter Wagner would agree and argues that the autopod is “a novel homolog without any antecedent in any fish fin” (p. 160). Moreover, the challenge for evolutionists is surely compounded when it is considered that there are also “fundamental differences” in the embryonic development of autopods in different tetrapods, i.e. salamanders, frogs, and amniotes (p. 163). Furthermore, the pentadactyl limb is supposed to be proof of a pentadactyl common ancestor. But the creatures that evolutionists claim were the closest to this ancestor were not pentadactyl! E.g. *Acanthostega* was octadactyl, *Ichthyostega* was heptadactyl, and *Tulerpedon* was hexadactyl, and they were rough contemporaries.

### Epigenetics and self-organisation

Denton discusses the demise of the increasingly discredited ‘gene-centric’

view of life, i.e. that DNA is the sole or primary determinant of higher organic form. Rather, genes generally “act as suppliers of the material needs of [embryonic] development ... [but not] as ‘controllers’ of developmental progress and direction” (p. 253). Genes do not provide a complete set of instructions for building an organism, and this is made clear by the discovery that their ‘meanings’ are context dependent, being determined to a significant degree by the environment in which they are expressed. Just as the

“English sound ‘rite’ may mean a variety of things from a direction to a legal term depending on the context ... [so] the cytoplasmic context in which the gene is expressed acts downwardly on the ‘gene’ to confer upon it biological meaning” (p. 254).

Amazingly, genes are regulated not just by the biochemical state of the cell but also by its physiology. For example, even the mechanical tension of the cell membrane can influence gene expression (p. 255).

It is becoming increasingly evident that self-organisation plays a major role in determining both cellular architecture and higher embryonic order. For example, while genes specify the components of a red blood cell’s membrane, its biomechanical properties give rise to the cell’s final biconcave form (p. 258) (figure 1). The mammalian photoreceptor is one of the most complex cells in the human body and its genetic blueprint is one of the most thoroughly documented of any metazoan cell. Interestingly, Denton argues,

“No genes or genetic elements have been identified which can be construed as having a specific morphogenic role ... The evidence suggests that the cytoarchitecture of the retinal photoreceptors, although enormously complex, arises from the self organization of the cell’s constituents without any regulation or direction from

an external genetic blueprint” (p. 259).

Moreover, there is growing evidence that biomechanical and biophysical forces, acting beyond anything specified by genes, actually sculpt embryos (p. 261).

Denton believes that evolutionary novelties were generated by similar epigenetic and self-organising principles. However, while he argues convincingly that these play significant roles in embryonic development, he presents no empirical evidence that they could direct the process of ‘molecules to man’ evolution. Rather, his argument is based on ‘the fact of evolution’ and the implausibility of Darwinism. He writes,

“... what *natural* explanation, what directive natural force is available other than natural law? What explanation other than the fitness-structural paradigm, which sees the forms of life as no less built into nature than the properties of water [emphasis in original]?” (p. 278).

In his thinking, only natural causes can be invoked to explain the existence of the living world and, since cumulative selection has failed, self-organisation must provide the answer.

According to Professor Andreas Wagner,<sup>9</sup> “complex macroscopic innovations, such as the evolution of new body parts, may involve changes in the regulation of multiple molecules, and the evolution of new molecules. Known macroscopic innovations are so complex that we do not yet understand all required changes for any of them.”<sup>10</sup> Is it really plausible that self-organising natural laws with such creative abilities have remained hidden from scientists for over a hundred years?

## Conclusion

In *Evolution: Still a Theory in Crisis*, Denton shows conclusively that “*Nature is in fact a fundamental discontinuum of distinct Types and not*

*the functional continuum maintained by Darwinian orthodoxy* [emphasis in original]” (p. 219). At the same time he demonstrates, beyond all reasonable doubt, the inadequacy of cumulative selection as an explanation for the living world. However, his contention that complex organisms evolved by natural laws governing the self-organisation of matter has no more of a scientific basis than the neo-Darwinism he so effectively refutes.

According to Denton,

“If cumulative selection has no functional continuums to traverse gaps ... [e]ither the ‘jump’ was ... due to internal causal factors according to a structuralist ‘laws of form’ framework... or it came about as the result of special creation” (p. 229).

Sadly, he appears to adopt the former explanation simply because he rejects the latter *a priori*. Indeed, the book might be better titled *Neo-Darwinism: Still a Theory in Crisis*, as at no point does he question the reality of ‘molecules to man’ evolution.

## References

1. Denton, M., *Evolution: A Theory in Crisis*, Adler & Adler, MD, 1985.
2. Mehler, A.W., Richard Goldschmidt’s monster, *J. Creation* 16(2):42–45, 2002; [creation.com/images/pdfs/t/j16\\_2/j16\\_2\\_42-45.pdf](http://creation.com/images/pdfs/t/j16_2/j16_2_42-45.pdf).
3. Mazur, S., *The Altemberg 16: An Exposé of the Evolution Industry*, North Atlantic Books, CA, 2010.
4. Mazur, ref. 3, p. 34.
5. A superfamily within the order Coleoptera (beetles) containing numerous species with very long antennae.
6. A clade is a grouping that includes a common ancestor and all the descendants (living and extinct) of that ancestor.
7. Gould, S.J., The return of hopeful monsters, *Natural History* 86(6): 22–30, 1977.
8. Woltering *et al.*, Conservation and divergence of regulatory strategies at *hox* loci and the origin of tetrapod digits, *PLoS Biology* 12(1), 21 January 2014; [plosbiology.org](http://plosbiology.org).
9. Andreas Wagner is a full Professor at the Institute of Evolutionary Biology and Environmental Studies, University of Zurich.
10. Wagner, A., *The Origins of Evolutionary Innovations: A Theory of Transformative Change in Living Systems*, Oxford University Press, p. 14, 2011.



# A look into *The Unseen Realm*

***The Unseen Realm: Recovering the supernatural worldview of the Bible***

Michael S. Heiser

Lexham Press, Bellingham, WA, 2015

Lita Cosner

Many people see the Old Testament as a strange book that's hard to interpret. Many Christians neglect its study for that reason. Heiser argues that the key to understanding many of the 'difficult passages' in the Old Testament is recognizing the supernatural worldview of its authors. He makes sweeping claims about the potential effects of his research:

"What you'll read in this book will change you. *You'll never be able to look at your Bible the same way again* [emphasis in original]" (p. 13).

Central to that worldview, he argues, is the idea that Yahweh created spiritual or 'divine' beings with a variety of different roles. The 'sons of God' are his heavenly council, and human beings were originally intended to be His council on earth. That plan was temporarily derailed when the serpent, a disgruntled member of Yahweh's council, tempted Eve and caused the Fall. The rest of the Old Testament is the account of heavenly and earthly rebellion against Yahweh and His continuing plan to restore the earth and have mankind as His family on earth.

## Countering practical materialism

Today, many people in Western society no longer believe in God, angels, or other spiritual powers, while the existence of these entities would

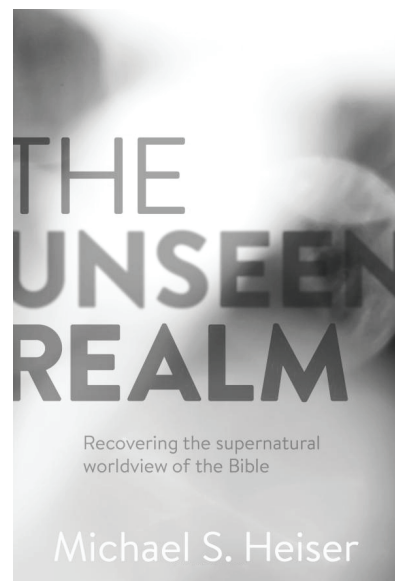
have been simply assumed in ancient times, and used to explain all sorts of phenomena. Even many Christians live as practical materialists, acknowledging God and the spiritual realm, but not believing that it has much of an impact on our daily life.

Heiser argues that if we are going to understand the Old Testament, we need to adjust our worldview. The Israelites lived in a world where the spiritual battle lines were clearly drawn between Yahweh, the God of Israel, and the lesser, corrupt gods who were given control of the other nations descended from Noah and his sons.

However, it is unclear how historically Heiser views the first chapters of Genesis. He believes that Genesis only reached its final form during the Babylonian exile (a common view among liberal Old Testament scholars). Therefore he regards some key passages, such as the Nephilim account in Genesis 6, were written as polemics against Babylonian religious practices. However, this is problematic because Jesus assumed Mosaic authorship of the Pentateuch, which was the unanimous view of Judaism and Christianity until modern times.<sup>1</sup>

## God's two households

One of Heiser's main arguments is that God has a council of created heavenly beings with a hierarchy. The highest ones in the hierarchy are called 'sons of God', and are his 'family in heaven' by virtue of their being created by Him. He does not need a council, but He chooses to use them (just as He does not need human beings, but chooses to use us). Some of these council members became corrupt, which is the reason why God sentences them to die as men in Psalm 82.



Heiser claims that seeing the divine council in Genesis helps to shed light on what happened in the Garden of Eden, which Heiser argues was the seat of Yahweh's divine council on earth. Heiser argues that the serpent was a member of the divine council who was unhappy with God's decision to make humanity in His image, and so orchestrated their rebellion against God. When he promised Eve that she would gain insight as a result of eating the fruit, he did *not* promise that she would become like Yahweh. Rather, he claimed that she would become like one of the *elohim*—one of the members of the divine council.

After the Flood, God covenanted with Noah and his sons, and commanded them to fill the earth. But after the rebellion at Babel, Heiser argues that Yahweh in essence disinherited the nations, assigning them to the authority of the lesser council members who became corrupt. Instead, He chose for His own people a nation that did not yet exist—Israel, through whom God would retake the nations.

One place Heiser missteps is when he argues that the Satan in Job is not the devil, but a member of the divine

council performing the task assigned to him.

“The *satan* described in these passages is not the devil. Rather, he’s an anonymous prosecutor, as it were, fulfilling a role in Yahweh’s council—bringing an accusatory report.” (p. 56)

It is true that Satan does not become the proper name of the devil/serpent until the New Testament, but one could argue that it is partially *because of Job* that it became his name. And Revelation seems to clearly identify Satan, the serpent, and the devil as the same entity. The figure in Job opposes God and wishes harm on someone who loves God, which is very consistent with Satan.

### God's mountain paradise

Combining Genesis 2 with Ezekiel 28, Heiser makes the case that Eden was a mountain garden, which makes sense of ancient Near Eastern conceptions of mountains as the dwelling of the gods. Seen this way, Babel becomes a human attempt to build another mountain paradise and thereby ascend to Heaven. It was not simply disobeying the commandment to spread out over the earth; it was overt rebellion.

### The seed of the serpent

Heiser believes that there were descendants of the Nephilim, called Anakim and Rephaim, in Canaan when the spies came back. Rather than concluding that the spies were lying about their presence, Heiser argues that they really were there and were only wiped out in David’s day.

However, the only time when the word ‘Nephilim’ is connected with the Anakim is in the spies’ lying report in Numbers 13:33. While Scripture continues to reference people of unusual stature up through David’s day, the Anakim are never explicitly

affirmed to be descendants of the Nephilim. And if the Nephilim were all killed in the Flood (and Genesis affirms that only Noah and his family survived) and the angels who fathered them were imprisoned until the day of judgment (2 Peter 2:4–8 and Jude 6–7), one wonders how the Nephilim could have reappeared. It seems much more likely that the spies genuinely encountered some large people, but to ensure that Israel refused to take the land they exaggerated their report even more and said that these people were actually descended from the Nephilim.

### A covert mission of salvation

Heiser also argues that there was a very good reason no one expected Jesus to be the sort of Messiah He was: the messianic prophecies were fragmentary and scattered throughout the Old Testament in such a way that we can only see their fulfilment in Christ in hindsight. Heiser argued that God did it this way to keep Satan in the dark. One might suppose that’s also the reason that Revelation is similarly difficult to interpret (as evidenced by the many interpretations of the book).

Heiser complains that Christians read the New Testament into the Old and this colours our perception of how the Old Testament authors would have viewed the text.

“These Old Testament passages and others have been made by modern commentators to speak about the messiah and his work in ways the New Testament authors *don’t* claim” (p. 243).

But if the New Testament authors were interpreting the Old Testament typologically, then believers today should also be able to look at the Old Testament in the same way and see connections, since the NT doesn’t claim to *exhaustively* catalog OT typology. Of course, our typological readings need to be responsible, and they’re

never authoritative as the NT typology is; however, there is no reason to limit the typology to that explicitly stated in the NT.

### Jesus, the unique Son

Heiser shows how the Old Testament seems to include two Yahweh figures—one invisible and one visible who appears to people in various times and places and is called the Angel of Yahweh or the Word of Yahweh. They are sometimes distinguished, and sometimes their identities are blurred together. Heiser argues that the Angel of Yahweh is the pre-incarnate Son of God. This is consistent with John’s revelation of the Logos (Word) who was both with God and God Himself (John 1:1–3).

Similarly, he argues that the identities of Jesus and the Holy Spirit are blurred in the same way in the New Testament (citing Acts 16:7, Romans 8:9, Galatians 4:6, 1 Peter 10:11). However, I think he is wrong in this assertion. Calling the Holy Spirit ‘the Spirit of Christ’ or ‘the Spirit of Jesus’ simply recalls Jesus’ promise that:

“... the Helper, the Holy Spirit, whom the Father will send in my name, he will teach you all things and bring to your remembrance all that I have said to you” (John 15:26).

Heiser is outright mistaken with claims using language that would delight modalist heretics, “The Spirit is Yahweh, and so he is Jesus as well.” However, Heiser redeems himself somewhat by stating the correct doctrine: “It is clear that Jesus and the Spirit are different persons” (p. 294). It is correct that the Old Testament does not teach the full Trinitarian doctrine. Rather, at that stage of God’s progressive revelation, the doctrine had not been revealed, but it was in no way contradicted. But the New Testament is fully Trinitarian, i.e. reveals that in

the one true God, there are precisely three Persons.

### Troubling inconsistencies

If Heiser had come to the text as a convinced inerrantist and a young-earth creationist, his book would have been much stronger and better. When it comes to the existence of spiritual beings, Heiser's concern is to get back to the original view of the biblical authors. Yet that same view would have included creation in six ordinary-length days and a global flood. And in places, one is unsure how *historical* Heiser views the events in Genesis 1–11 to be.

Heiser has a pleasant to read, accessible writing style. He breaks down complex ideas to make them understandable to people who can't read Hebrew and the other relevant ancient languages. This ability to communicate is sadly rare among Bible specialists. One only wishes he was a little more consistent in his goal to communicate the original worldview of the Bible.

### References

1. See Sarfati, J., *The Genesis Account*, Creation Book Publishers, Atlanta, GA, pp. 9–11, 2015.

## Atheist fantasies vs fact

### *Faith vs Fact: Why Science and Religion Are Incompatible*

Jerry A. Coyne

Viking Press, New York, 2015

John Woodmorappe

Jerry A. Coyne is a professor at the Department of Ecology and Evolution at the prestigious University of Chicago. (I know some professors and students there, and it is commonly regarded as one of the finest research universities in the world.) As soon will become obvious, this poorly thought-out book is inconsistent with what one would expect from such a prestigious university.

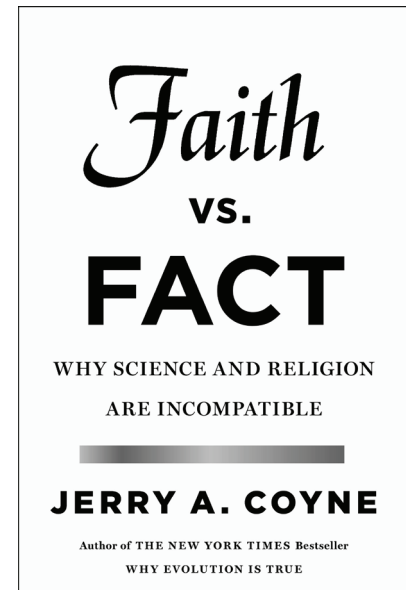
Although Coyne is a scientist, most of his book is on the philosophy and sociology of religion. The major theme of this book is that there is no evidence for the factuality of anything paranormal or supernatural, and that that is why scientists stick to naturalism, which does not demand an *a priori* assumption (e.g. p. 93). However, Coyne never explains what kind of evidence he, or other scientists, would find convincing. It sounds as if no evidence would ever being sufficient.

### Coyne's flippant thinking

The informed reader will quickly realize the superficiality of this book. Here are just a few examples.

To begin with, author Jerry A. Coyne recounts his background:

“And a bit more biography is in order: I was raised a secular Jew, an upbringing that, as most people know, is but a hairsbreadth from



atheism. But my vague beliefs in God were abandoned almost instantly when, at seventeen, I was listening to the Beatles' *Sergeant Pepper* album and suddenly realized that there was simply no evidence for the religious claims I had been taught—or for anybody else's either. From the beginning, then, my unbelief rested on an absence of evidence for anything divine” (p. xiii).

Amazing! All it took was one song to wipe out the 17 year-old Coyne's however-tentative belief in God. And he complains that those who accept the existence of God are shallow thinkers!

The author jumps to conclusions with effortless ease. For instance, he mentions some experiment in which a brain scan shows a signal a few seconds before the person is consciously aware of making a decision (pp. 15–17). Presto! Free will has been disproved. Better still, the capacity of humans choosing to freely accept their Savior, and to choose right from wrong, also has been disproved.



I could not help but think of Mark Twain, who said, “There is something fascinating about *science*. One gets such wholesale returns of conjecture out of such a trifling investment of fact.” As everyone familiar with neurobiological data can attest, the way a brain ‘lights up’ is amenable to different interpretations.

Coyne’s statements about Scripture are no better. He glibly asserts, for example, that there is no evidence for the Exodus (pp. 90, 258). More on Coyne’s fledgling understanding of the Bible later.

The author delivers standard jibes against creationists (p. 104). They are so ludicrous, and so outdated, that I will not dignify them with a response.

### A decisive blow against religious compromise

To his credit, Coyne rejects the “all religions are basically the same” notion, pointing to the fundamental and irreconcilable differences between religions. He also rejects the “Bible is metaphor” concept, pointing to the tendency to ‘allegorize’ Scripture in order to escape conflicts with science. He also debunks those who invoke Augustine and Aquinas to justify their

compromise. He quotes from these luminaries to show that a figurative interpretation of Scripture does not replace a literal one. In fact, figurative interpretations *presuppose* the validity of the standard literal interpretations! (pp. 57–58).

What are scientific creationists up against? The reader may be struck by how well funded are the forces of evolutionary compromise. For example, the wealthy Templeton Foundation funds BioLogos, which, in the words of Coyne, “is designed to show evangelical Christians that they can accept both Jesus and Darwin” (p. 19).

Coyne at least finds creationists more grounded in reality than compromising evangelicals and other accommodationists. He quips:

“Sometimes it seems that scriptural literalists are more intellectually honest than the ‘scripture is not a textbook’ crowd, who, rather than admit that science has falsified much of the Bible—and, by implication, has cast doubt on the rest of it—argue that the book is effectively one long parable. After a stiff dose of pick-and-choose apologetics, the words of the Australian creationist Carl Wieland seem like a gust of fresh air” (p. 75).

### Evolutionistic faith in action

This is how Coyne imagines (and I stress *imagines*) the presumed evolutionary origin of life:

“We know it happened between 4.5 billion years ago, when the Earth was formed, and 3.5 billion years ago, when we already see the first bacterial fossils. And we’re virtually certain that all living creatures descended from one original life-form, for virtually all species share the same DNA code, something that would be a remarkable coincidence if the code arose several times independently. But because the first self-replicating organism was small and soft-bodied and thus could not fossilize (it was likely a molecule, perhaps surrounded by a cell-like membrane), we don’t have a way of recovering it” (p. 37).

Ah, that poignant, child-like faith of the evolutionist! (See figure 1.) And Coyne complains about religious believers accepting the factuality of something that they cannot see and things that cannot be tested! What’s more, Coyne complains about theists engaging in falsification-proof reasoning and falling back on dogmatism. Ironic, to say the least!

Not surprisingly, Coyne repeats the rationalist dictum that “Extraordinary claims require extraordinary evidence”. Just as non-surprisingly, he exempts atheist ideas from such a standard of scrutiny. From his quoted statement, above, it is obvious that there is no evidence—let alone extraordinary evidence—that life came about from non-living chemicals. But what does it matter? The atheist believes anyway. That is all he has.

But wait. Coyne is not finished yet. Faced with the problem of the fine-tuned universe making life possible, he conjures up hypothetical exotic forms of life that don’t require a fine-tuned environment, perhaps based on silicon or—better yet—not even based

# Atheism

The belief that there was nothing and nothing happened to nothing and then nothing magically exploded for no reason, creating everything and then a bunch of everything magically rearranged itself for no reason what so ever into self-replication bits which then turned into dinosaurs.  
Makes perfect sense

Figure 1. Just some of the untested beliefs of the atheist

on matter (p. 162). Isn't Coyne's logic wonderful? He will not believe in an unseen spiritual God but is prepared to believe in an unseen 'spiritual' form of life!

The author characterizes the multiverse theory as follows:

"Now, it's not clear whether we can actually show that there are multiple universes, for they might be undetectable from our own. Still, physicists are beginning to devise ways to test their existence, and we've recently seen evidence for at least one of their preconditions: cosmic inflation" (p. 163).

Regardless of whether or not either or both the multiverse and God are testable, the former of which he affirms and the latter of which he denies, we see once again Coyne's bottomless atheistic evolutionary faith in action.

In common with many other evolutionists, Coyne laments the fact that much of the American general public does not accept evolution. Perhaps this is, first and foremost, because the evidence for molecules-to-man evolution is so weak that even the layperson can see through it.

### Evolution and testability

The author repeats the contention that the ultimate claims of religion are not testable while evolution is testable—in that evidence could be found to disprove it. In actuality, evolution is so plastic that it, in practice, is not susceptible to potential falsification. Any observation could be fitted into it. Permit two examples raised by Coyne (p. 31).

Coyne repeats the stock argument about a mammal fossil, found in Paleozoic strata, disproving evolution. It would not. *Ad hoc* modifications of phylogenies happen all the time. Stratigraphic-range extensions—including spectacular ones—also happen frequently. So, if a mammal

was found in the Paleozoic, evolutionists would just recast their ideas in terms of mammals evolving earlier than previously supposed, and having a polyphyletic origin—one in the Triassic and an unexpectedly earlier one in the Paleozoic. After all, science is full of surprises, and science always changes in the face of new discoveries.<sup>1</sup>

He also claims that an adaptation in a species that is only relevant for another species—such as a pouch found on a wallaby that gives birth to fully-developed placental babies that need not go through a pouch-dwelling stage of development—would disprove evolution. It would not. The evolutionist would simply say that here is an unusual marsupial mammal that has—only recently—evolved a placental-style fully developed neonate at birth, enabling it to skip the pouch-dwelling stage. Not enough time has elapsed for the pouch to disappear, or at least become vestigial, in the mother. To make the foregoing scenario more intellectual-sounding, he would probably say that evo-devo predicts the rapid emergence of major changes in living things caused by an evolutionary 'tweaking' of the rate of ontogenic development.

Pointedly, this very reasoning that Coyne imagines would falsify evolution actually exists in evolutionary thinking! Humans have generally irrelevant adaptations, 'aquatic' ones, which would be suitable to another, aquatic, species. Humans have several adaptations, such as near-hairlessness, face-to-face copulation, high body fat, and bipedalism, that are non-existent or rare in non-human primates. This has led to the aquatic hypothesis, which posits that a branch of ancestral primates had started evolving to an aquatic lifestyle, but something changed, and that is why humans are stuck with a number of aquatic adaptations even though they are not aquatic.<sup>2</sup>

Any conceivable biological observation can be assigned an evolutionary explanation. If there is selfishness in nature, this is intuitively obvious. But if there is altruism, it must be because of kin selection. But what happens when neither individual fitness nor group fitness are at stake? Here Coyne, once again, engages in the kind of auxiliary hypotheses that he is fond of accusing religionists of doing:

"Animals that have their own litters will often adopt members of another species. ... This happens because the 'adoption' option simply isn't common in nature, and natural selection has operated to promote the suckling of infants that happen to be nearby—which are almost invariably your own" (pp. 175–176).

So much for the testability of evolution.

### Why are leading scientists almost all atheists?

Rejection of God is fundamentally a spiritual problem, and it afflicts intellectuals the most. This has long been known (1 Corinthians 1:25–27).

Coyne claims that, of all ID (Intelligent Design) proponents that he knows, only David Berlinski is not motivated by religion. If true, so what? How many evolutionists, especially ardent ones, are motivated by atheism, if only subconsciously?

The author cites some studies showing that scientists are much more likely to be atheists than the American general public. As for elite scientists—members of the National Academy of Sciences—the disparity reaches staggering proportions. Fully 93% are atheists or agnostics and only 7% believe in a personal God (p. 12). From this, Coyne concludes that the more scientifically minded a person is, the more likely he/she appreciates the lack of evidence for the supernatural. However, not to be

denied the 100% that he would like to have, he disparages the 7% who do believe in God as engaging in compartmentalized thinking. How self-serving!

Most concerning of all, Coyne does not consider alternative explanations for the foregoing trends. To begin with, advancement in academia, such as the granting of tenure and the election to the National Academy of Sciences, are not solely based on scholarly merit or the quality of one's thinking. They are, in part, a popularity contest. Internal politics also plays a role, as does the 'fit' of the candidate to the culture of academia.

Let us analyze all this. Could it be that atheistic scientists are more likely to be elected to the National Academy of Sciences because they are a better match to the secular ethos of academia? Could even intellectual snobbery play a role—in that those scientists who reject the ways of the 'ignorant masses' (read: religion) are more likely to be esteemed by their peers, and thereby elected to the National Academy?

For the sake of argument, however, let us assume that election to the National Academy of Sciences is based on high-level scientific merit and nothing else. Could it be that those who will not accept God gravitate to science because its inquisitive and skeptical character makes it easier for them to rationalize their rejection of God and His authority? More specifically, could it be that atheists are especially abundant in the disciplines of biology and psychology (p. 13) because these very fields are the most effective ones in making one feel successful in one's evasion of God? Finally, could it be that the most intelligent scientists are the ones most likely to be atheists because—by the very fact of their powerful intellect—they are

the ones most in need of cultivating a highly developed scientific mindset for the purpose of rationalizing their highly cognizant rejection of God?

But let us go beyond religion. Consider the fact that scientists (especially elite scientists) usually reject not only God, but also *anything* non-material (such as *any* form of life after death). Does the exercise of the scientific method tend to make scientists materialists or do people who have a materialistic mindset (what-we-see-is-all-that-matters) tend to gravitate to modern uniformitarian science precisely because of its materialistic outlook? One could think of the psychologist Maslow's hammer: if you are a hammer, then everything to you is a nail.

### Straw-man believers

The author complains about straw-man arguments. Ironically, he is consistently the worst offender.

Coyne cites evidences that most religious believers are that way because of upbringing or emotion, not reason. However, exactly the

same could be said of most atheists—most of whom were either raised with little or no religious grounding or are rebelling against God for some reason (sinful lifestyle, bad experiences with religious believers, personal tragedy, perceived unanswered prayer, etc.)

Now consider science itself. How many scientists accept what they believe (e.g. evolution) because they have weighed the evidence in depth for themselves, and have genuinely become convinced of its correctness, and how many believe out of a spirit of conformity with prevailing scientific opinion? Coyne repeats the mantra that science, unlike religion, encourages doubt, and that science treats questioning as a virtue instead of a vice. This is a half-truth, as evidenced by the many untoward experiences that dissenting scientists had experienced in the past. If nothing else, this can include the denial of funding for research.

In attempting to show how 'scientific' those of his ilk are, Coyne asserts that scientists freely accept disproving evidences, and contrasts this with some prominent believers who have said that no evidence could ever convince them, for example, that the Resurrection of Jesus Christ never happened. Excuse me, but how many atheists would never believe in God no matter what? (I have heard of atheists who say that, were the sky to open up and were they to see God face-to-face, they would sooner believe that they had a psychotic episode than they would admit the reality of God.)

Now consider disproof in science itself. Coyne points out that the Piltdown Man hoax was exposed by scientists, but conveniently fails to mention that it had been an amateurish forgery, and that it had taken only 50 years for the hoax to be exposed. This, and other



**Figure 2.** A biologically-irrelevant adaptation is said to falsify evolution, yet such adaptations exist in nature.



significantly persisting scientific shenanigans that could be mentioned, does not exactly inspire confidence in the premise that science particularly encourages disproof.

### Straw-man Christianity

The author repeats the claim that what religion one practises is primarily an accident of birth. This is a half-truth. To begin with, isn't being an atheist also usually an accident of birth? Barring consideration of God's will (which determines the advantages and disadvantages of every person ever born: Acts 17:26), there is one sobering reality: very many things (such as one's gender, race, socio-economic status, the capabilities and character of one's parents, and time in history one lives in) are also accidents of birth. The vast majority of Christians alive today had ancestors that were pagans. In virtually every culture and clime, there have been individuals who have come to the One True God. Finally, being born in a nation with the one true religion is no guarantee of being a faithful practitioner of that religion.

Coyne lumps all the miraculous claims of all religions into one and the same bag. To Coyne, one account of a miracle is as much non-factual as any other claim of a miracle. That is like saying that because some written events are legendary, therefore all written events are legendary.

The author consistently cites only evidence that supports his atheistic contentions. For instance, he claims that scientific experiments have disproved the efficacy of prayer, while ignoring other experiments that at least suggest the efficacy of prayer. Of course, the one who rejects God can always fall back on rationalizations, such as a poorly controlled experiment, the seemingly all-powerful power of

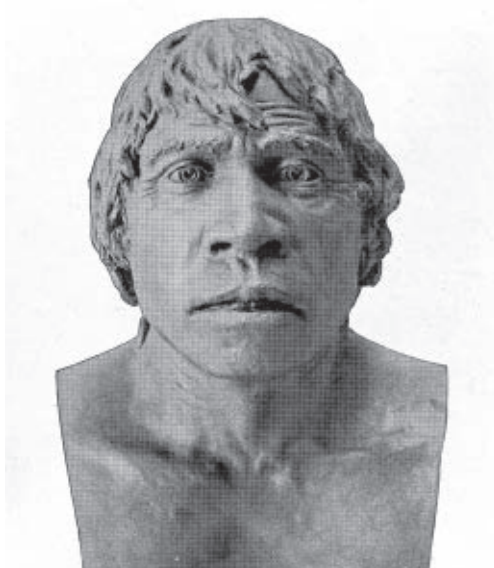
suggestion acting on the one praying, etc.

Coyne's understanding of the evidences for the Christian faith is indefensible. He does not demonstrate even a rudimentary understanding of the evidences for the historicity of the Gospels and Epistles. He engages in dismissive hand-waving, and repeats the trite statement that the Gospels were written some decades after the events—as if this was *ipso facto* supposed to invalidate them (e.g. p. 121). If such reasoning were applied to the factuality of Julius Caesar, described long after his death, it would also surely be disproved. Predictably, he dusts off the so-called contradictions between the Gospels on the Resurrection accounts, but does not tell the reader that these divergences are superficial, are hardly any different from those in different newspaper accounts of the same event today, and are exactly what one would expect to see when comparing independent sources.

Not done yet, Coyne, in dead seriousness, repeats the most ill-informed counter-explanations for the

Resurrection of Jesus Christ (p. 123). This includes the charge that the disciples invented the Resurrection, in 'collaborative storytelling', as a means of dealing with the cognitive dissonance of seeing their leader die. This was supposed to be comparable to the way that modern cults deal with disconfirming events, such as the failure of the world to end as predicted. Coyne's facile explanation is just that. If Jesus just died, why did the disciples not deal with the cognitive dissonance of His death through more prosaic, standby explanations—such as their lack of faith, their being found unworthy by God, or God's ways being mysterious? Conversely, if the human mind is simultaneously so creative and irrational in dealing with cognitive dissonance that it can fabricate an elaborate bodily resurrection, then what can it NOT do? Must the historian worry, for example, that Julius Caesar and his exploits never happened, and were merely the 'collaborative storytelling' in response to some kind of event that had caused cognitive dissonance in ancient Rome?

The author repeats the silly argument that certain Christian doctrines were determined by vote (pp. 70–71). In actuality, the Council of Nicaea did not invent the doctrine of the Trinity. Nor did it impose this belief on the church. Coyne fails to mention the fact that the overwhelming majority of votes at Nicaea affirmed the full Deity of Jesus Christ, thus proving the fact that the Trinity had long been pre-existing mainstream Christian doctrine. The Arian heresy had been an upstart movement, and had been unambiguously dealt with. The Trinity had been re-affirmed, and Arianism exposed and condemned. There was nothing that needed to—much less had to—be 'imposed' upon the church.



**Figure 3.** The Piltdown Man hoax, an amateurish forgery that took only 50 years to unmask, does not exactly inspire confidence that science is fundamentally skeptical of its findings.

## Disparaging Christianity and the origins of modern science

Predictably, Coyne repeats the line about early European scientists being Christians solely because almost everyone was a Christian. His logic is self-refuting. If the Christian religion is especially toxic to scientific reasoning, then why did science develop, and persist, of all places, precisely in the one in which confessedly almost everyone was a Christian?

The author boldly asserts that European science does not owe its origins to Christianity. However, he states that “In the end, we don’t know why modern science arose for keeps in Europe between the thirteenth and sixteenth centuries, while arising and then vanishing in China and Islamic countries” (p. 215). Without actually getting into the evidences for the crucial role of Christianity in the foundation of science, let us just analyze Coyne’s logic. It, once again, is self-refuting. If Coyne cannot know why science persisted in Europe, unlike in other places, then how can he so boldly say that Christianity had nothing substantial to do with it?

### ‘Science has good intentions’

Not surprisingly, Coyne glosses over all the evil consequences of Darwinian evolution. He would have us believe that eugenics and racism were simply corruptions of Darwinism brought upon us by racists and xenophobes (p. 219). This is laughably untrue. Racism and eugenics were no add-ons to, or misuses of, Darwinism. They had been given the imprimatur of scientific legitimacy by 19<sup>th</sup>-century ‘science’, had been part of the very fabric of Darwinism, and had been actively researched and promoted by leading Darwinists, moreover, for many decades after 1859.

Coyne realizes that both religion and science have done bad things, and that one theoretically could

blame bad policy makers, rather than religion or science *per se*, for this. Not to be denied, however, he insists that religion has an inherent propensity for wrong, owing to its dogmatic insistence on knowing the truth. However, the ‘inherent propensity for wrong’ argument can also be applied to science. The scientific-knowledge spirit can easily corrupt to an intellectual hubris, leading to a ‘we know a lot’ or even ‘we know what is best for you’ mentality, sometimes ending in disastrous policies.

Continuing his diatribe against religion, Coyne repeats the idiotic cliché that religion is unique in its ability to make good people do evil things. I beg pardon. How many murderers in the Soviet NKVD had been good people, convinced by an atheistic ideology (Communism), that their killing of class enemies was a necessary and noble deed—a favour to human progress?

Coyne also asserts that science, unlike religion, at least strives for correction owing to its self-testing nature, even if it is sometimes mistaken to the point of being harmful. This is a variant of the ‘we have good intentions, so excuse us’ argument. However, this ‘good intentions’ argument can also be applied to religion. When the Inquisition tortured heretics, it did so not because religionists are mean and petty. The Inquisition’s actions were based on the good intention of saving souls and preventing sin from spreading. When the mostly religious authorities limited or abolished the Inquisition, and introduced religious tolerance, it was based on the good intention of not stifling legitimate differences and dissent, and the good intention of not causing the suffering of those who believed differently. Note also, the Spanish Inquisition killed about 2,000 people over three centuries.<sup>3</sup> This pales into comparison with the genocidal *Holodomor* (Голодомор, ‘murder by starvation’), where millions of Ukrainians died

in the man-made famine of Stalin’s atheistic Communism in 1932–1933.

Failing all else, Coyne insists that science has made dramatic progress, while religion remains static. That premise, of course, depends upon his narrow materialistic definition of progress. In science, progress is measured in terms of discoveries, inventions, and an enhanced standard of living. In the Christian faith, progress is measured in leading successive generations of people to devotion to God.

## Conclusions

I personally appreciated Coyne’s book in a way. It enabled me to see afresh the folly of the atheist position and the desperation of its attacks on religious believers.

However, I would not recommend this book to the serious student of science and religion. Coyne says nothing new, much less anything profound. This book is so superficial and repetitive that it eventually becomes tedious to read. It is one shallow tired cliché after another. Coyne repeatedly complains about religious believers accepting things that they cannot see and test, but has no problem in believing in unseen and untested things so long as they fit his atheistic evolutionary preconceptions.

## References

1. Doyle, S., Precambrian rabbits—death knell for evolution? *J. Creation* 28(1):10–12, 2014.
2. Bergman, J., The Aquatic Ape Theory: challenge to the orthodox theory of human evolution, *J. Creation* 21(1):111–118, 2007.
3. Kamen, H., *The Spanish Inquisition: A Historical Revision*, Yale University Press, 1999.

## Catastrophic plate tectonics and plate tectonics—a comparison of two theories

I feel some clarification is in order after reading Mark McGuire's recent article entitled "Catastrophic plate tectonics and plate tectonics—a comparison of two theories".<sup>1</sup>

First, his article seems to follow the same format of most anti-catastrophic plate tectonics (CPT) articles, pointing out minor, unresolved issues in the overall theory, yet offering little in a viable alternative.<sup>1</sup> Many of these articles merely proceed with criticism of CPT as if little data in support of CPT actually exists.

Since the 1960s, the geologic literature has been filled with data supporting horizontal movement of lithospheric plates, some obviously more valid than others. In contrast, there is a despairingly obvious lack of published alternative (non-CPT) explanations for: (1) the mantle tomography showing clear and continuous oceanic lithosphere subducted beneath trenches (figure 1)<sup>2</sup>; (2) the heat flux pattern across ocean ridges that supports sea-floor spreading; (3) the differences in magma chemistry observed at volcanoes in locations like Hawaii, Italy and the USA West Coast that can be best understood using the CPT model; and (4) the linear patterns of earthquakes, volcanoes and mountain ranges that are so readily explained by plate boundaries. Just how do the alternative hypotheses explain these empirical data?

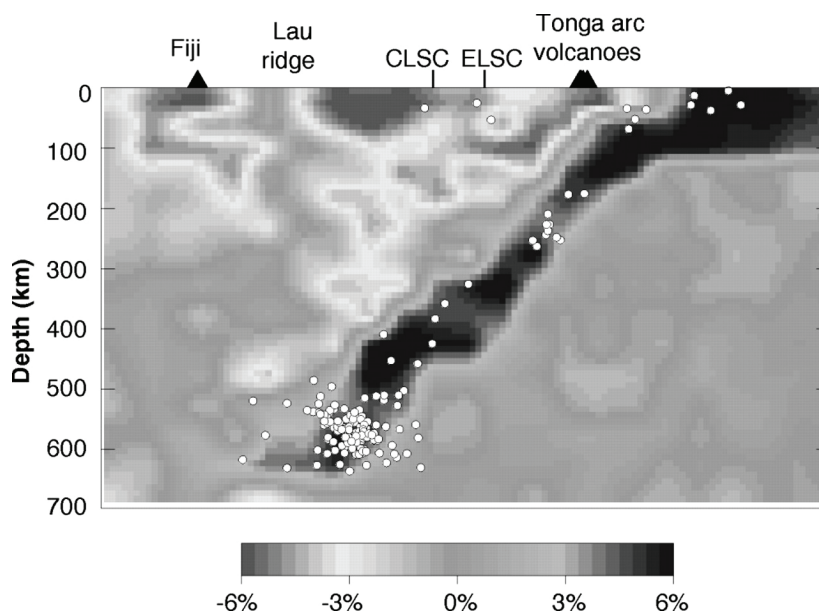
Criticism of CPT is fine. It is a theory. It does not have the answers to every issue, and likely never will.

However, creation scientists should examine all the relevant data and choose the best explanations that follow the truth of Scripture. I personally believe CPT offers the best biblically based explanation for the entire spectrum of observable geologic data. Other authors may disagree, but they cannot disregard empirical data. We cannot reach any sort of Flood model consensus if we exclude available data from our thinking.

One final thing I would like to clarify was discussed by McGuire on page 106 and in endnote number 32 on page 112.<sup>1</sup> It seems that McGuire, and possibly others, believe that CPT involves two complete subduction cycles which consumed the entire oceanic lithosphere twice. I believe this is incorrect. Yes, John Baumgardner has previously pointed out that there is a lack of so-called Paleozoic-age oceanic lithosphere in existence today. However, his unpublished computer model suggests only a minimal amount of Paleozoic oceanic lithosphere was created during the Flood, mostly in the South Pacific.<sup>3</sup> He also found that subduction

in the South Pacific seemed to cease at the end of the Paleozoic. My own unpublished research fits this interpretation also. I find minimal coverage of the continents with Flood sediments during the Paleozoic megasequences. It is not until the latest Paleozoic and into the Mesozoic that I find the most extensive sedimentary coverage of the continents. This implies a greater amount of ocean crust was being produced in the Mesozoic and, likewise, less during the Paleozoic.

All this to say that most supporters of CPT do not advocate the subduction of two complete ocean surfaces between days 40–150 as McGuire assumes.<sup>1</sup> I don't think there ever was a claim in CPT to subduct 669 million km<sup>2</sup> of ocean surface into the mantle during the Flood. The amount subducted was more likely not appreciably greater than the original, pre-Flood ocean surface, or closer to 360–400 million km<sup>2</sup>. Finally, there was not only subduction activity during the Flood around the ring of fire (40,000 km), there was subduction along southern Europe,



**Figure 1.** East-west profile of P-wave velocity across the subduction zone beneath the Tonga island arc volcanoes, Pacific Ocean. Earthquakes caused by subducting slab shown with small circles. Velocity perturbation scale shown at bottom. (From Zhao *et al.*<sup>2</sup>, figure 2.)



the Middle East and even northern India that McGuire didn't include in his estimate.<sup>1</sup> These locations add another 15,000–20,000 km to the length of worldwide subduction during the Flood event. When you add in the proper numbers, the result does fit inside the mantle.

Timothy L. Clarey  
Dallas, TX  
UNITED STATES of AMERICA

### References

1. McGuire, M., Catastrophic plate tectonics and plate tectonics—a comparison of two theories, *J. Creation* 29(3):104–112, 2015.
2. Zhao, D., Xu, Y., Wiens, D.A., Dorman, L., Hildebrand, J. and Webb, S., Depth extent of the Lau back-arc spreading center and its relationship to the subduction process, *Science* 278: 254–257, 1997.
3. Baumgardner, personal communication, 2015.

### » Mark McGuire replies:

First of all, I would like to thank the editors of *Journal of Creation* (*JoC*) for publishing the two articles on uniformitarian plate tectonics (UPT) and catastrophic plate tectonics (CPT). *JoC* has presented ideas like this in the past (whether they agree with the author's position or not) which promotes healthy debate. Second, when I read the book *The Genesis Flood*<sup>1</sup> in 1980, I was convinced that Whitcomb and Morris presented a valid Flood model which included vertical tectonics (VT) based on the Bible verse “The mountains rose; the valleys sank down ...” (Psalm 104:8). The UPT/CPT model may explain oceanic crust better than VT, but the VT model explains mountains better than the UPT/CPT model. This is a matter for debate. Also, it was the study of oceanic crust which elevated the plate tectonics (PT) model to its dominance today.<sup>2</sup>

Next, concerning topics in the letter to the editor, the intent of the two previous articles<sup>3,4</sup> was to point out problems in the UPT/CPT models which need to be addressed. I started

researching this topic in 2012 and I discovered in almost every area there is some issue that needs explanation. A paper of this size limits what can be discussed so several of the major ‘icons’ of the PT model—subduction zones and the bending of plates, the San Andreas Fault, and magnetic striping—were highlighted. But, many other areas could have been chosen such as intra-plate tectonics (the New Madrid Fault) or mountain building<sup>5</sup> (the Alpine system in Europe and Africa was only briefly mentioned in these articles) or hot spot tracks (how the Hawaiian-Emperor island chain ‘jumped’ from one direction to another).

As for empirical data, we all have the same data but that data must be interpreted. Mantle tomography is subject to interpretation. There are at least three different interpretations that cause the relative velocity variation:

1. thermal differences between hot and cold slabs,
2. density differences between lithosphere,<sup>6</sup> and
3. chemical depletion rather than temperature variation.<sup>7,8</sup>

Moreover, on examining the Tonga Trench and Tonga and Fiji island tomographic section (assuming thermal differences), it appears that the main heat flow from the subducting slab is between the Tonga and Fiji

islands yet there are no volcanic islands at that location. Also, there appears to be a heat-flow connection to the Tonga islands but not Fiji. How did the Fiji islands form without a connection to the subduction zone, and why are there no island arcs over the main heat source? As far as subduction (subsidence) zones are concerned, they could be explained in the VT model as a semi-infinite beam loaded at its edge (figure 1).

Also, I would like to clarify that the calculation used to determine the length of the subducting slab was based solely on the Pacific Ocean. The area for the Pacific Ocean is 166,242,000 km<sup>2</sup>. The subduction zones in the Pacific ring of fire is 40,000 km. These were the numbers used to calculate the 4,160 km length. I apologise for the confusion.

Furthermore, one of the problems of writing these articles was where UPT/CPT models differ. In the UPT model, plate movement has been going on since at least the Cryogenian Period which is approximately 650 Ma in the uniformitarian model.<sup>9</sup> It should be noted that one of the problems with any period prior to the Cambrian is the lack of fossils, and without fossils it is almost impossible to date the time period. The final breakup of Pangea took place around 200 Ma. Whether CPT follows this reasoning was not clear and I assumed that it would.

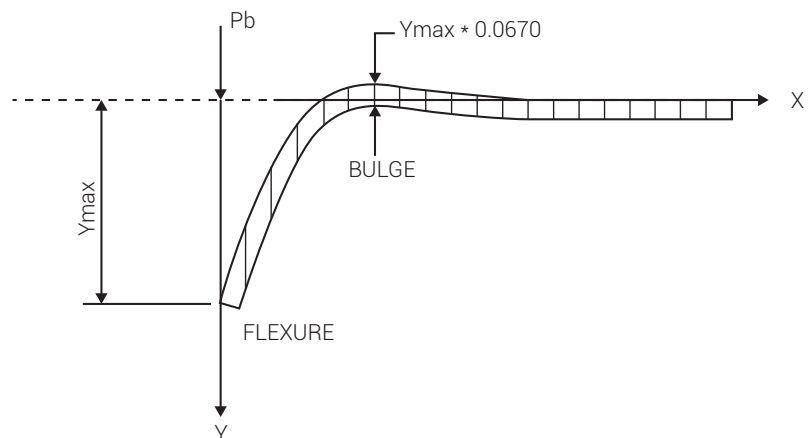


Figure 1. Flexure of a semi-infinite beam based on the equation  $Y = (Y_{\max})e^{-\lambda x} \cos \lambda x$  (after Watts<sup>10</sup>)

In any model there is going to be a question as to what the pre-Flood earth looked like. However, if it does not follow the UPT model then that distinction needs to be made.

Finally, I would like to say I commend the work of John Baumgartner and his colleagues and I pray for him and many other creation scientists and the organisation they represent on a daily basis. I do not agree with the CPT position but I certainly think that the creationist community has benefitted from his work as a counter argument to the UPT model.

Mark McGuire  
Memphis, TN

UNITED STATES of AMERICA

## References

- Whitcomb, J. C. and Morris, H.M., *The Genesis Flood*, Presbyterian and Reformed Publishing Company, Phillipsburg, NJ, 1961, 35<sup>th</sup> edn, pp. 121–122, 1991.
- Belousov, V.V., Certain Trends in Present-day Geosciences, *Critical Aspects of the Plate Tectonics Theory, Volume I*, Theophrastus Publishing and Proprietary Co, Athens, Greece, pp. 3–15, 1990; pp. 6–9.
- McGuire, M., Plate tectonics—inconsistencies in the model, *J. Creation* 28(2):104–115, 2014.
- McGuire, M., Catastrophic Plate Tectonics and Plate Tectonics—a comparison of two theories, *J. Creation* 29(3):104–112, 2015.
- Ollier, C.D. and Pain, C., *The Origin of Mountains*, Routledge, London, UK, 2000.
- Boyd, O.S. and Sheehan, A.F., Attenuation Tomography Beneath the Rocky Mountain Front: Implications for the Physical State of the Upper Mantle, *Geophysical Monograph Series* 154, 2005; colorado.edu/geosci/faculty/pdf/GM01036ch27\_Boyd.pdf.
- Yuan, H. and Dueker, K., Upper Mantle Tomographic Vp and Vs Images of the Rocky Mountains in Wyoming, Colorado and New Mexico: Evidence for a Thick Heterogeneous Chemical Lithosphere, [geofaculty.uwyo.edu/dueker/PAPERS/agu%20monograph%20cdrom%20tomography%20yuan.pdf](http://geofaculty.uwyo.edu/dueker/PAPERS/agu%20monograph%20cdrom%20tomography%20yuan.pdf).
- Choi, D.R. and Vasiliev, B.I., Geology and tectonic development of the Pacific Ocean: part 4. Geological Interpretation of Seismic Tomography, NCGT Newsletter, no. 48, September 2008, pp. 52–60; p. 52; [ncgt.org/newsletter.php](http://ncgt.org/newsletter.php).
- Gradstein, F.M., Ogg, J.G., Schmitz, M.D. and Ogg, G.M., *The Geologic Time Scale 2012*, vol.1, Elsevier BV, Oxford, UK, p. 43, 2012.
- Watts, A.B., *Isostasy and Flexure of the Lithosphere*, Cambridge University Press, New York, pp. 102–108, 2001.

## Creationism in Europe

I find myself significantly at odds with Jerry Bergman's rather positive review of a recent multi-authored book on the status of creationism and intelligent design in Europe.<sup>1</sup> On the surface of it, I acknowledge that the book, titled *Creationism in Europe*, appears to be a well-structured, crisply written summary of an interesting subject. However, from my own knowledge of the European biblical creation scene, some of the authors have failed to do their research properly, relying extensively on secondary (even disreputable) sources.

Regrettably, I must disagree with Bergman's glowing assessment of the book: "a well-documented review" and "an excellent, fairly balanced review of the situation of Darwin Doubters in Europe". The following selected examples should suffice to illustrate my concern (quotations that follow are from the book itself rather than Bergman's review):

*United Kingdom* (chapter 3, pp. 50–64). "British creationism has ... had very little impact on public debate in the school system." On the contrary, the last decade and a half have seen a number of high-profile discussions arise concerning the 'threat of creationism' regarding children's education. Humanist and secular groups in the UK have lobbied the Department of Education to change policy and have largely succeeded in restricting the freedom of creationist speakers to visit schools, even upon invitation.<sup>2</sup> The author of this chapter has leaned heavily upon the BCSE for his information—the so-called *British Centre for Science Education*—a blog site which exhibits appalling scholarship by any standard.<sup>3</sup> Even anti-creationist Richard Dawkins has ridiculed BCSE's founder, describing him as a liar and a 'self-promoting fool'.<sup>4</sup> In the author's discussion concerning creationist organisations,

*Creation Science Movement* (formerly *Evolution Protest Movement*)<sup>5</sup> is said to be connected to *Biblical Creation Ministries* (it is not), which is said to be the "second largest creationist organisation in Britain".<sup>6</sup> Most other active groups, even small ones, are covered, but *Creation Ministries International* is nowhere mentioned in this chapter about UK creationism.<sup>7</sup> For many years, CMI has had an especially active, country-wide (not to mention Europe-wide) speaking ministry and hosts one of the world's most prominent creationist websites ([creation.com](http://creation.com)). CMI's *Darwin: the Voyage that Shook the World* documentary film, screened country-wide in 2009, stirred up sufficient controversy for the BBC to interview one of the film's evolutionist interviewees alongside a CMI representative. One must conclude that the author of this chapter (Joachim Allgaier) and the three editors of the book as a whole—the subject of Bergman's review—had very little (if any) knowledge of the UK creation scene and were wholly reliant upon secondary sources, failing to adequately research their subject matter.

*Germany* (chapter 6, pp. 105–124). In this chapter, Werner Gitt is discussed briefly on a single page; he is described as an 'engineer' and a co-author (with six other writers) of a 2009 book published by a Swiss society. There is no mention of his important work in Information Science. Gitt is among the most prolific German creationist authors (including translations into other languages) but this fact is also overlooked.

*The Netherlands* (chapter 4, pp. 65–84). Having, myself, spoken in this country on many occasions, I was disappointed in the apparently selective reporting and ignorance exhibited by the three writers of this chapter. The focus is on Intelligent Design (and also theistic evolution); there is no mention whatsoever of

‘*Mediagroep in Genesis*’ (MiG; previously known as *Workgroep in Genesis*), which began around 2004 and grew in prominence. They promoted a number of national speaking tours with CMI’s Philip Bell and AiG’s Terry Mortenson (with the national press sometimes showing interest) and have a successful website. Moreover, MiG encouraged publication of Dutch translations of a good number of books and DVDs.

Bergman writes that the book “is a well-documented review of the status of creationism in 10 European countries”. However, it seems that his main source of information was the book itself rather than first-hand knowledge of the situation in Europe. He does mention that the authors are “all Darwinists or ex-creationists”; indeed, Ronald L. Numbers wrote the Foreword, a man whose apostasy from a former profession of faith hardly qualifies him as an impartial observer. Apparently, Numbers’ own book on creationism was well-researched,<sup>8</sup> but Sarfati wrote:

“... his prejudices are evident. The book majors heavily on personalities, with subtle (and some not-so-subtle) character assassinations, while the high scientific qualifications of many creationists are downplayed. He invariably gives the last word to the evolutionist, which often leaves an impression contrary to the facts as can be seen upon checking the sources.”<sup>9</sup>

In my view, Numbers’ endorsement of *Creationism in Europe* and the authors’ own worldview obligations warrant much more caution. An ‘important reference’, as Bergman describes it? Not without independent corroboration from established creationists in those same 10 European nations.

Philip Bell  
Leicester  
UNITED KINGDOM

## References

1. Bergman, J., Review of: *Creationism in Europe*, Blancke, S., Hjermslev, H.H. and Kjærgaard, P.C. (Eds.), Johns Hopkins University Press, MD, 2014; *J. Creation* 29(3):33–36, 2015.
2. See, Statham, D. and Bell, P., Dawkins gloats over boost to evolutionary dogma in schools, [creation.com/dawkins-bha-schools-creation](http://creation.com/dawkins-bha-schools-creation), 21 January 2012; also, Statham, D., Evidence for Creation now banned from UK religious education classes, [creation.com/creation-religious-education](http://creation.com/creation-religious-education), 19 July 2012.
3. BCSE Revealed, Blog by David Anderson, last updated February 2008; [www.bcse-revealed.info/bcse/bcse.rev/Main/HomePage.html](http://www.bcse-revealed.info/bcse/bcse.rev/Main/HomePage.html), accessed 4 February 2016.
4. Anderson, D., Atheist spat: the New Atheists vs their bedfellows in the NCSE/BCSE, [creation.com/bcse-and-ncse-in-atheist-spat](http://creation.com/bcse-and-ncse-in-atheist-spat), 24 May 2010.
5. Munday, E., The British Evolution Protest Movement: a brief history, *Creation* 8(2):41–42, 1986; [creation.com/evolution-protest-movement](http://creation.com/evolution-protest-movement).
6. In January 2016, it was announced that *Biblical Creation Trust* had been formed from the amalgamation of three UK creationist organisations: *Biblical Creation Society*, *Biblical Creation Ministries* and *Genesis Agendum*.
7. Though a different author of chapter 7, on Poland, does mention “almost fifty articles” translated into Polish on [creation.com](http://creation.com).
8. Numbers, R., *The Creationists: The Evolution of Scientific Creationism*, University of California Press, CA, 1992.
9. Sarfati, J., The Yellowstone petrified forests, *Creation* 21(2):18–21, 1999, reference 12.

## » Jerry Bergman replies:

The goal of the book *Creationism in Europe* was to review the creation movements and those involved. Philip Bell’s response to my review indicates that he thought the book should be a very different book, namely a review of the problem of discrimination against creationists. At the least Bell’s response added to the book *Creationism in Europe*, although at times contradicted it. He found some errors, but in my experience of reading scores of anti-creation books, most are replete with errors and inaccuracies. I am very familiar with the often irrational antagonism against those who oppose the Darwinian worldview. I have, so far, written six books documenting the problem, namely *Slaughter of the Darwin Dissidents*, *Silencing the Darwin Dissidents*, *Censoring the Darwin Dissidents*, *Suppressing the Darwin Dissidents*, *Eminent Scientist Darwin Doubters*:

*Nobel Laureates and other Eminent Scientists who have rejected Orthodox Darwinism*, and *Four Times a Heretic*. Each of these books has over a thousand footnotes documenting the claims made in the book.

In my book review, I was comparing *Creationism in Europe* to those books written on the subject of creationism from a secular viewpoint, and, in general, I found *Creationism in Europe* to be far less inaccurate and vociferous, but much of the secular literature on creationism is often so antagonistic and inaccurate that this may not be saying much. The secular literature on creationism is so filled with *ad hominem* arguments and name calling that I have devoted an entire chapter to this topic in my *Silencing the Darwin Dissidents* book.

Common claims in many secular books imply that Darwin doubters, as a whole, are retrogressive, ignorant, loons, liars, and even child abusers. In contrast, *Creationism in Europe* contained a fair amount of positive material about the movement, as well as brief discussions about some of the creationist opposition. It could have contained more objective information about the opposition; but as I document in my book *Censoring the Darwin Dissidents*, if it was obviously pro-creation, it probably would not have been published by a mainline secular publisher. My review was on the contents of the *Creationism in Europe* book, and I assumed the authors were usually fairly accurate when this was not always the case.

I have six file cabinets documenting the situation in the United States, and only about one file drawer documenting the situation in Europe. Thus, I welcome Mr Bell’s letter to help correct both my knowledge gaps and, more important, the research of the authors of the book at issue here. I encourage Mr Bell to complete the research required to document in detail the situation in Europe. I will be honoured to include a chapter or two by him in volume seven of the



series described above that carefully documents the situation in Europe.

My book *Slaughter of the Darwin Dissidents* was rejected by every publisher that I sent the manuscript to, both secular and Christian. The reason was either that they concluded that my claim was true—creationists were facing widespread discrimination, and that discrimination is appropriate because creationists are a threat to science; or that my claims were not valid—creationists are not facing discrimination but falsely claiming persecution that does not exist. As I was writing this I ran across the following comment in an email message in reaction to my work in this area: “Bergman is again touting his bogus claim that those who reject the modern science of Darwinism are discriminated against.”

When I finally found a publisher, the book sold close to 4,000 copies, and it is now out in a second edition. This is a respectable number, since most academic books typically sell close to only 1,000 copies. The over 40 reviews, including those on Amazon, were, almost without exception, very favourable. Several supporters purchased copies to donate to academic libraries, many of which refused to place the book on their shelves. Examples include Bowling Green State University and Wheaton College in Wheaton, Illinois. Ironically, Bowling Green State University had on its shelves my first book covering this topic, namely, *The Criterion; Religious Discrimination in America*.<sup>1</sup>

Even several Christian creation groups refused to carry my books on this topic, explaining that it was negative and they wanted to leave the impression that creation was a respectable scientific activity. (I need to add that CMI has consistently strongly supported my work.) Frankly, I was surprised that *Creationism in Europe* was published by a major secular academic publisher, and wonder how many times it was

rejected by potential publishers. Following its acceptance by Johns Hopkins University Press, I wonder how much editing by the publisher occurred. If it had included the material that Mr Bell cited, I doubt very much it would have been published.

In summary, Mr Bell’s response suggests that he had wanted Johns Hopkins University Press to publish a very different book than *Creationism in Europe*. It is like complaining that a book titled *The Role of Darwinian Eugenics in Nazi Germany* almost totally ignored the many military battles fought during the second World War. If Mr Bell was disappointed that *Creationism in Europe* was a very different book than he expected, I strongly encourage him to write that very different book. Furthermore, I will do what I can to ensure that this very different book is published and widely distributed. It is sorely needed, and no competition exists that I am aware of.

Jerry Bergman  
Montplier, OH

UNITED STATES OF AMERICA

## References

1. Onesimus Publishing Co., Richfield, MN, 1984.

## Cnidarians turn evolutionary theory into jelly

The article “Cnidarians turn evolutionary theory into jelly”, on p. 74 of issue 29(3), contains helpful and relevant information, especially about jellyfish genes. However, I’d like to offer a clarification about what author Jean O’Micks wrote regarding jellyfish fossils. He argued that preservation of original jellyfish tissue defies the fossils’ deep time age assignments.

O’Micks wrote, “Tentacles and muscles have been shown to be preserved among these specimens.” I read the paper he referenced (Cartwright *et al.*, *PLoS ONE* <sup>1</sup>) in order to better understand the nature of this preservation. Cartwright *et al.* did not specify whether the plainly visible jellyfish body parts were preserved as mineralized (i.e. body tissues replaced by minerals) or original, but really old, body chemicals, like proteins. Not having access to the fossils or any means to chemically test the preserved portions, I’m left to speculate about the nature of their preservation.

They occur in Cambrian System strata, and original tissue fossils from the Cambrian seem to be extremely rare. I know of only one with unambiguous biomolecular preservation, and it comes from Canada’s Burgess Shale.<sup>2</sup> According to my limited understanding, Burgess-type fossils typically show body part preservation as mineralized—often by pyritization or keratinization—and flattened residues.<sup>3</sup> Sometimes, differential mineralization will produce various colours for different fossil body tissues. Cartwright *et al.*’s *PLoS ONE* images show various colours within jellyfish specimens, so these may well be mineralized. Once they are in place, of course, minerals can last much longer than original biomolecules, so they form no basis for a creationary argument that they defy evolutionary age assignments.

Thus, Jean O’Micks seems not to have distinguished between endogenous molecular preservation in fossils, for example the endogenous collagen in dinosaur bone that his Bertazzo *et al.* reference demonstrated, with *mineralized preservation* that appears most often in Cambrian fossils. But there’s a big difference. Cartwright *et al.* give no evidence for (or against) molecular preservation in the Cambrian jellyfish described in *PLoS ONE*. Unfortunately, this typifies

the literature, where researchers show much more interest in trying to trace evolutionary relatedness of new body forms than in analyzing fossil chemistry (or biochemistry). Thus, Jean O'Micks' concluding statement on p. 78, "Preservation of jellyfish tissue over such supposed long periods of time is thus highly improbable" is irrelevant since no such evidence has been demonstrated for these Cambrian Jellyfish. I found most everything else about his paper very insightful.

Brian Thomas  
Dallas, TX  
UNITED STATES of AMERICA

### References

1. Cartwright, P. *et al.*, Exceptionally preserved jellyfishes from the Middle Cambrian, *PLoS ONE* 2(10):e1121, 2007.
2. Ehrlich, H. *et al.*, Discovery of 505-million-year-old chitin in the basal demosponge *Vauxia gracilenta*, *Scientific Reports* 3:3497, 2013, DOI: 10.1038/srep03497.
3. Thomas, B., Original Biomaterials in Fossils, *Creation Research Society Quarterly* 51:234–247, 2015.

### » Jean O'Micks replies:

I thank Brian Thomas for his question regarding my paper about jellyfish fossils. It is certainly important to distinguish between soft body tissue and mineralized fossils.

In response, I would like to state that the original paper that was cited (Cartwright *et al.*) mentions that all fossils are from the Marjum Formation, Middle Cambrian, Utah, the Sponge Gully Locality, and that this locality also yields soft-bodied biota and trilobites. Thus, other soft-bodied specimens exist besides the one Mr Thomas mentions from the Canadian Burgess Shale, so there is a possibility that this specimen is also soft-bodied.

Regardless, I think that since jellyfish have extremely soft tissues it would be quite remarkable that anything would remain of them long

enough to become mineralized. To me, it seems that even if the jellyfish have indeed been mineralized, it would have to have been due to rapid burial, which is something we would expect to have occurred during Noah's Flood.

Jean O'Micks  
Omaha, NE  
UNITED STATES of AMERICA

## Examining the floating forest hypothesis: a geological perspective

I read with interest Timothy Clarey's article on the floating forest hypothesis.<sup>1</sup> I found myself in agreement with some of his conclusions but partly for reasons outside those aspects addressed by the paper. May I briefly explain and ask for comment?

One of the prime links I see in the paper is to explore the possible relationship of the forests to the coal deposits in the 'Carboniferous' and its paucity elsewhere, e.g. 'Cambrian'. We are conditioned to think of coal as a fossil fuel. Because its feedstock is organic matter, including wood and peat followed by a thermodynamic metamorphic process called 'coalification', it is biogenic.<sup>2</sup> This quoted uniformitarian process requires huge volumes of feedstock and long periods of time. Even then there are gaps in explaining the rich variety of 'macerals' (the individual combustible contents similar to minerals) in coal. Creationists have focussed on the volume and time issues. Floating forests offer an explanation for large

amounts of precursor material that could have existed before the Flood. Also, they have shown that some aspect of 'coalification' proceed rapidly so that we end up with a model that explains coal in geographically related multiple layers.

While secular/uniformitarian literature in general believes that coal is biogenic, some have challenged this and that challenge introduces a new level of enquiry for creationists. The late Professor Thomas Gold pointed out 10 reasons why coal could not be biogenic, and suggested that it was abiogenic and had arrived from Earth's depths by an out-gassing molecular fusion process.<sup>3</sup> He was challenged on several fronts, including the incompleteness of his model, but we might ask which scientific model is ever fully complete, including the biogenic coalification model? Second, he was not a trained geologist. He had worked on radar in WW2, and then with Sirs Fred Hoyle and Herman Bondi on cosmology at the time when the steady state model of the universe reigned supreme. This suggests an *ad hominem* attitude to his views on the origin of coal.

In addition to his 10 objections, we encounter at least another 15 implicit objections to the biogenic origin for coal from a wide range of specific journals and books, although no alternative abiogenic models are even suggested. The objections are: the complexity of the vitrinites (which are key macerals since, for example, they form 90% of Turkish coals<sup>4</sup>), inconsistent rank correlation, mineral-ash content, tonstein layers, variability of sulphur content, coal balls, appeal to Gaia, dinosaur footprints in mines, low pre-Cambrian plant availability, lateral persistence of seams, flat-topped seams, general shortage of carbon, seat earths, radio-carbon in coal, divergence and reconnection of split seams, washouts and roof roll-overs. Within this short comment we

cannot go into technical details, but, as a minimum, surely they prompt a fundamental reconsideration?

Some creationists attempt to explain geological features of the Flood by searching for ways of speeding up the timescales implied by uniformitarians. Thus they essentially retain the geological column, plate tectonics, reaction kinetics assumptions and everything else as has been done by many authors who have contributed to the floating forest-to-coal model. The other route is to anchor each aspect of our models directly on the biblical information and build from there, only embracing uniformitarian ideas when all the evidence points that way. The contrast between the two has been explored by Froede and Akridge<sup>5</sup> and the subsequent discussion.<sup>6,7</sup> But truth is not either/or. It is one or the other.

There is a close parallel between the origin of coal and that of crude oil. During my 30 years in the upstream oil industry I was all too conscious that the origin of oil was not clear-cut. While the majority of professionals accepted a biogenic option, as they did for coal, typically 30% accepted Gold's other idea, namely that oil is

abiogenic. Major industry conferences failed to settle the issue.<sup>8</sup>

I wrote a paper<sup>9</sup> that showed the major problems with both options, and offered a new model. It borrows ideas from Gold, but avoids the problems he encountered with entrained fossils and his vague 'upwelling' process because these are dealt with within an active Flood environment. The thermodynamic issues of a short timescale and the vexatious question of oil migration disappear. The model I offered also avoids one of the key problems with the 'biogenic' model that no biogenic feedstock is known to replicate the full range of known compositions of crude oil, particularly in the lower numbered alkanes and the waxes. (This has a close analogy with the problem of explaining the wide range of macerals in the 'biogenic' coal model.) Secularists have challenged my model, not on the physics and geology but only because it uses biblical Flood timescales. De facto, what is the alternative for creationists?

Gold's and the other 15 objections to coal being biogenic provide us with the initiative to seek the origin

of coal without using woody material as a feedstock. While the ideas of floating forests (and perhaps log mats) have suggested explanations for the amount of carbon in the right place at the right time, the coalification thermodynamics and the sedimentary issues point to the need to look for a radical alternative, as was needed for oil. There are many pointers to coal being a precipitate discharged onto the surface of the earth from the fountains of the great deep during the Flood. The starting evidence is that some of the quite common vitrinites are known to be soluble.<sup>10</sup> It explains the sedimentary aspects of coal and fossil content replicating those of sandstone or limestone, which are not contentious for creationists.

Just as the oil industry formally accepts that a significant fraction of its scientists consider that oil might be abiogenic, are we neglecting the possibility that coal is abiogenic? We are not denigrating the effort creationists have put in developing biogenic models via floating forests and log mats, but, as in all aspects of science, it is only by making a wide search for explanations that we arrive at plausible models.

John D. Matthews  
Wool, Dorset  
UNITED KINGDOM

## References

1. Clarey, T.L., Examining the floating forest hypothesis: a geological perspective, *J. Creation* 29(3):50–55, 2015.
2. Krauskopf, K.B. and Bird, D.K., *Introduction to Geochemistry*, McGraw-Hill, New York, 1995.
3. Gold, T., *The Deep Hot Biosphere*, Copernicus, New York, 1999.
4. Karayigit, A.I. and Whateley, M.K.G., The origin and properties of coal seam associated with continental micritic limestone ... Turkey; in: Gayer R.A. and Pesek, J. (Eds.), *European Coal Geology and Technology*, The Geological Society, London, Special Publication No. 125, pp. 101–114, 1997.
5. Froede, C.R., and Akridge, A.J., A developing schism in Flood Geology, *J. Creation* 27(2): 49–54, 2013.
6. Ross, M., A developing schism in Flood Geology, *J. Creation* 27(3):46–47, 2013.



Used with permission of *Answers Magazine*<sup>2</sup>



7. Froede, C.R., and Akridge, A.J., reply to: A developing schism in Flood Geology, *J. Creation* 27(3):48, 2013.
8. Katz, R.J., Mancini, E. and Kitchka, A.A., A review of the AAPG Hedberg Research Conference on origin of petroleum—biogenic and/or abiogenic and its significance in hydrocarbon exploration and production, *AAPG Bulletin* 92(5):549–556, 2008.
9. Matthews, J.D., The origin of oil—a creationist answer, *Answers Research J.* 1:123–146, 2008.
10. Scott, A.C., Coal petrology and the origin of coal macerals: a way ahead? *Intl. J. Coal Geology* 50: 119–134, 2002.
11. Wise, K.P., Sinking a floating forest, *Answers* 3(40): 40–45, 2008

### » Timothy Clarey replies

The intent of my article was not to stir discussion on the biogenic or abiogenic origin of coal, or oil, for that matter. It was to point out some geological shortcomings of the floating forest hypothesis.<sup>1</sup> However, as the author of the comment asked for input, I will provide a brief contribution on this debate.

I personally believe the biogenic origin of coal is the most reasonable explanation of the scientific data available. We find many examples of plants associated with coal whether it is Carboniferous coal or otherwise. If coal were merely a “precipitate discharged onto the surface of the earth from the fountains of the great deep”, we would expect to find vast quantities of coal spread throughout the sedimentary record, including in the earliest Flood sediments or the Lower Palaeozoic rocks. The Bible clearly tells us that the fountains bursting forth were the first event in the Flood (Genesis 7:11). If the fountains provided the coal, where are the massive coal beds in the Cambrian, Ordovician, and Silurian system strata? Why do we find the vast majority of Palaeozoic coals only in the rocks of the Upper Carboniferous system (Pennsylvanian)?

Secondly, as a former employee of a major US oil company, I disagree that “a significant fraction of its oil industry scientists consider oil might be abiogenic”. The claim “typically

30% accepted Gold’s other idea, namely that oil is abiogenic” is not representative of what I witnessed in industry. This assertion is not based on any scientific survey, but is the opinion of the author of the above comment alone.

The recent American Association of Petroleum Geologists Hedberg Conference on the origin of petroleum concluded that “no single inorganic origin [for oil] has been proposed” and that “some of the inorganic mechanisms incorporated a biogenic step converting mantle-derived methane to heavier hydrocarbons, or coexisted with an organic process”.<sup>2</sup>

As other presenters at the conference pointed out from a study of oil and shale in the Williston Basin, US: “... the oil chemistry suggested the presence of three distinct oil types. Each of these oil types or families could be matched to extracts from a different stratigraphic interval—Winnipeg shale, Bakken shale, and Tyler shale—with each considered as a source interval.”<sup>3</sup>

The conference concluded that the inorganic hypothesis for oil formation did not provide a specific location where oil should be expected, adding little value in terms of oil exploration. In contrast, the conference determined that the supporters of the biogenic origin proposed a single petroleum formation mechanism, based on organic-rich source rocks. And that the “organic origin permitted an approach to exploration”.<sup>2</sup>

In addition, engineers at the US Department of Energy’s Pacific Northwest National Laboratory reported they were able to transform harvested marine algae into crude oil in less than one hour.<sup>4</sup>

If you combine the Williston Basin study, above, which chemically tied the oil produced to the source rock extracts (and numerous similar studies), with the empirical results of the US Department of Energy, it is

hard to deny an organic origin for the majority of the world’s crude oil.

As Flood geologists we shouldn’t have to be in awe at the amount of oil in the world. Global oil generation is another example of a process that could only have occurred because of the extraordinary burial conditions present during the recent great Flood. Most secular petroleum geologists deny the Flood, even though they are witness to this evidence every day as they search for oil. We can be thankful for God’s providence in creating oil, even through a catastrophic, global judgment—oil that now provides much-needed energy for our present world.

Timothy L. Clarey  
Dallas, TX

UNITED STATES of AMERICA

### References

1. Clarey, T.L., Examining the floating forest hypothesis: a geological perspective, *J. Creation* 29(3):50–55, 2015.
2. Katz, R.J., Mancini, E. and Kitchka, A.A., A review of the AAPG Hedberg Research Conference on origin of petroleum—biogenic and/or abiogenic and its significance in hydrocarbon exploration and production, *AAPG Bulletin* 92(5):549–556, 2008; p. 555.
3. Katz, Mancini, and Kitchka, ref. 2, p. 553.
4. Rickey, T., *Algae to crude oil: Million-year natural process takes minutes in the lab*, Pacific Northwest National Laboratory news release, posted on pnnl.gov, 17 December 2013, accessed 2 January 2014.

# The Ice Age as a mechanism for post-Flood dispersal

Timothy L. Clarey

The dispersal of the animal kinds to the various continents after disembarking the Ark is an important issue in any Flood model. Log mats have been proposed as a solution but may be less effective in transporting large animals, especially in light of potential post-Flood storms that would likely break up the vegetation mats. Land bridges seem to be a better solution for dispersal. This paper suggests that land bridges for animal and human migration were a consequence of the post-Flood Ice Age. The timing of the ice build-up, the lowering of sea levels and the dispersion at the Tower of Babel seem to have facilitated migration to the various continents. Advocates for a K/T or K/Pg post-Flood boundary have not sufficiently considered the difficulty of large mammal migration in their interpretations of the Cenozoic fossil record. The timing of the land bridges was no mere coincidence. The Ice Age seems to have been an integral part of God's plan to disperse the animals and humans to the separated continents.

For the past few years, creation scientists have been debating the Flood/post-Flood boundary with vigour.<sup>1–12</sup> One issue that seems to have been overlooked in this ongoing scientific debate is post-Flood animal migration. The Bible clearly tells us that humans stayed near the Tower of Babel, disobeying God's command to fill the earth for several generations after the Flood (Genesis 11:9).<sup>13</sup> “Meanwhile, the animals on the Ark had already fulfilled God's command to ‘abound on the earth, and be fruitful and multiply’ (Genesis 8:17).”<sup>13</sup> But, just how did the animals, and the large mammals in particular, get to the individual continents after the Flood waters receded?

In accordance with Catastrophic Plate Tectonic theory (CPT), the post-Flood configuration of the continents was likely vastly different from the pre-Flood arrangement (figure 1a).<sup>8,14</sup> Some sort of supercontinent configuration kept the major land masses together prior to the Flood.<sup>8,15</sup> During the Flood, the break-up of this supercontinent separated the individual land masses to the locations we see today (figure 1c). As Ross has pointed out, even if the pre-Flood continental configuration was identical to today, meaning there was no plate movement at all, we still attain today's modern post-Flood configuration.<sup>8</sup> However, neither of these scenarios resolve how large animals were able to get from the Ark landing site in Asia/Middle East to North America, South America, and Australia, now separated by vast distances of ocean water.

## Hypercanes and crumbling log mats?

Post-Flood floating log mats have been proposed as a mechanism for plant and small animal dispersal, but the duration time and thickness of the proposed log mats create

bigger problems for the larger animals.<sup>16,17</sup> Wise and Croxton assumed floating log mats and trees may have remained afloat for several centuries or longer after the Flood ended.<sup>16</sup> However, these assumptions were not based on empirical evidence. Instead, they based their duration estimate on the work of Steve Austin, who calculated a Douglas Fir flotation half-life of 75 years for the floating logs at Mount St Helens.<sup>16</sup> Austin also observed that most of the other plants sank even faster, with about half of the total vegetation mat sinking in just the first 20 years.<sup>18</sup> Considering such a short, measured half-life, projecting this out to ‘several centuries’ after the Flood seems a bit presumptuous.<sup>16,19</sup>

In addition, intense post-Flood storms and possible hypercanes, as modelled and proposed by Vardiman, would have likely caused the vegetation to sink more quickly.<sup>20</sup> Considering this scenario, the preservation of log mats that were extensive and dense enough to carry large animals seems less likely.<sup>21</sup> Mike Oard has pointed out: “Small herbivores comfortable with the water would most easily have survived voyages, but the primary factor would have been the resilience of the mat itself.”<sup>19</sup>

Larger mammals also need a greater source of fresh water. Supplying these large animals with sufficient fresh water, while floating on a vegetation mat for any length of time, remains an additional unresolved issue. Massive post-Flood storms would have also likely torn the floating mats apart repeatedly and prevented the build-up of any large freshwater ‘lakes’ atop (or even below) the floating mats, as suggested by Wise and Croxton<sup>16</sup> and Oard.<sup>19</sup> To date, the suggested solutions to this issue have been based more on speculation than on empirical data.<sup>16,19</sup>

There is little doubt that insects, small animals, and plants were able to disperse via vegetation mats, as described by

Wise and Croxton<sup>16</sup> and Oard.<sup>19</sup> Even secular scientists are beginning to admit the need for water dispersal, particularly for the island of Madagascar off the east coast of Africa.<sup>22</sup> But as Oard has stated: “Many of the animals on Madagascar are small and could have traveled with ease on a log mat.”<sup>19</sup> The transoceanic dispersal via ocean currents described by Wise and Croxton seems reasonable to explain fossil insects, lungfish, and small mammals, but inadequate for transport of the larger mammals such as elephants, camels, and horses. And both a male and female would be required to float to the same locations to populate any distant continent, making the likelihood of large mammal transport via log mats all the more improbable.

### Land bridges needed

How did the larger mammalian families get to their various continental locations after departing the Ark? The answer seems to be land bridges. Some sort of dry-land migration routes would have been needed to facilitate movement of the animals from the Ark site to the remote continents of the post-Flood earth, in accordance with God’s instruction to “abound on the earth and multiply” (Genesis 8:17). The Ice Age after the Flood provides just such an opportunity.

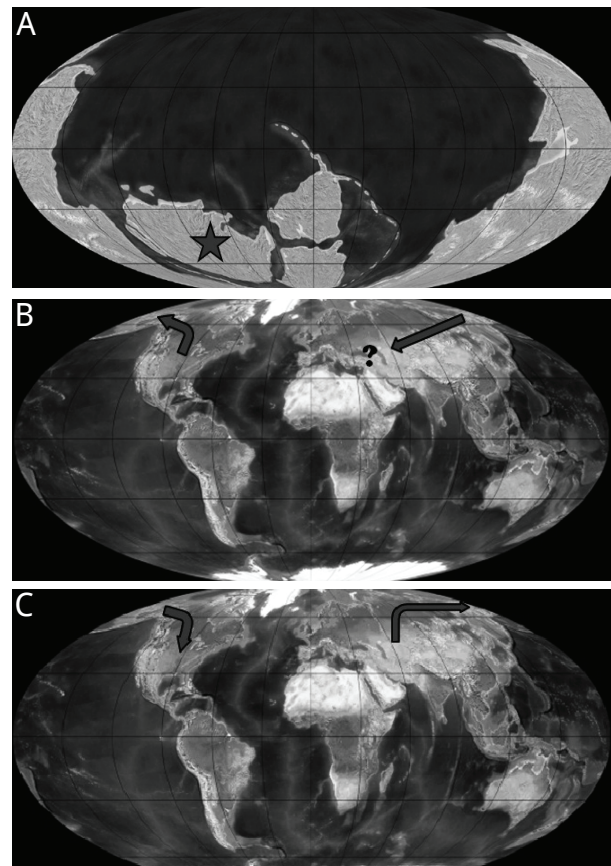
Immediately after the Flood, there would have been no ice caps.<sup>19</sup> This would have raised the post-Flood sea level by as much as 70 m above today’s level,<sup>23</sup> making it even more difficult to migrate from continent to continent immediately after the Flood. However, the build-up of additional ice as continental glaciers during the Ice Age would have temporarily lowered sea levels by another 60–85 m below even today’s level for a total sea level drop during the Ice Age maximum of as much as 130 m, depending on ice thickness estimates.<sup>2,24</sup> This 130 m includes the 70 m drop in sea level for the current glaciers in Greenland and Antarctica, and an additional 60+ m drop for the various continental glaciers during the Ice Age. The resulting land bridges would have made viable pathways for animals, big and small, to walk to the major continents (figure 2). These land bridges were formed as a consequence of the storage of water into massive continental ice sheets, causing a dramatic lowering of sea levels. Therefore, the Ice Age seems to provide the most practical way for the larger animals to migrate to all the continents.

Oard has further explained how hotter ocean temperatures could have kept the coastal lowlands of Siberia, Alaska, and the Yukon from developing thick glaciers during much of the Ice Age.<sup>24</sup> Warm oceans would have moderated the temperatures along the coasts and facilitated migration to the Americas and elsewhere by keeping temperate pathways open during much of

the Ice Age.<sup>24</sup> He estimated an initial post-Flood ocean temperature of 30°C and calculated the cooling rate of the oceans using heat balance equations. Oard concluded that the oceans would take close to 700 years to return to today’s temperatures, while a glacial ice maximum would be reached in about 500 years, post-Flood.<sup>24</sup> The warmer oceans and the formation of multiple ice caps would have preserved pathways along the coasts and possibly preserved gaps between the glaciers (figure 3).<sup>25</sup>

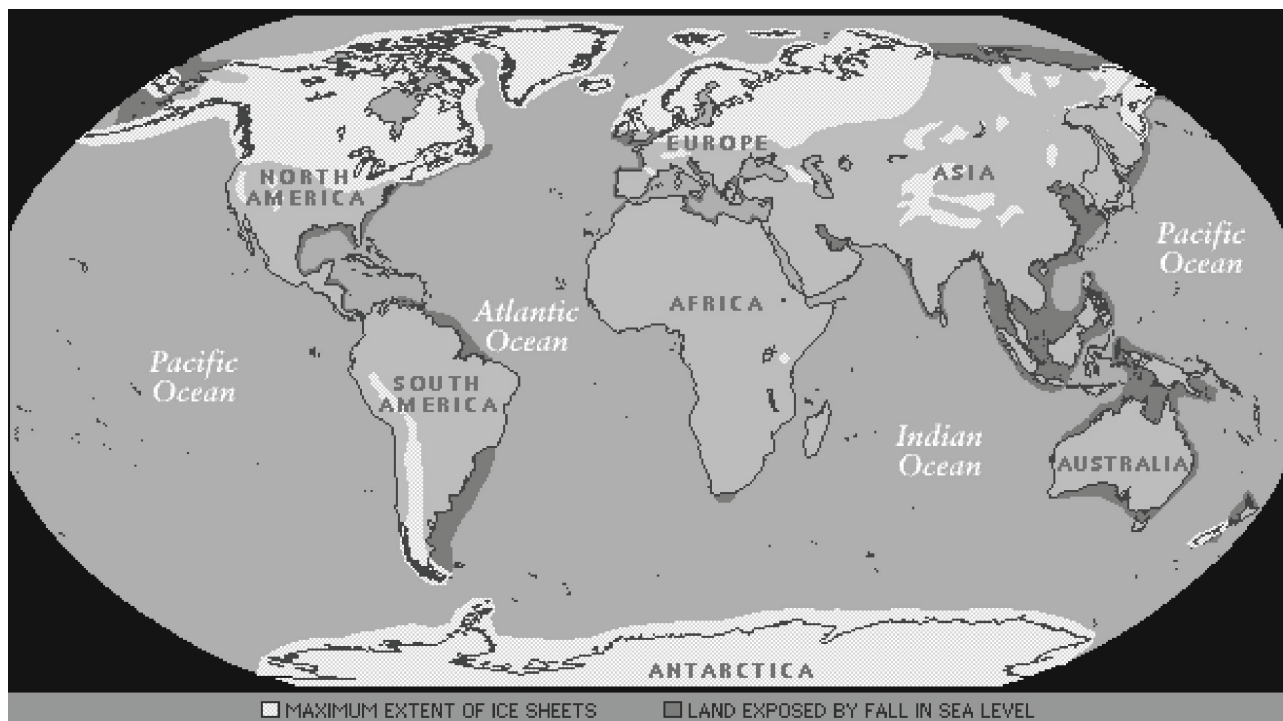
### Timing of the Tower of Babel and the post-Flood Ice Age

The timing of the Ice Age was no accident. Oard’s explanation of high post-Flood ocean temperatures and intense late-Flood volcanic activity seems to adequately explain the Ice Age.<sup>24</sup> And his calculation that the glacial maximum and a simultaneous maximum drop in sea levels could have been achieved about 500 years after the Flood seems reasonable.<sup>24</sup> The resultant, temporary land

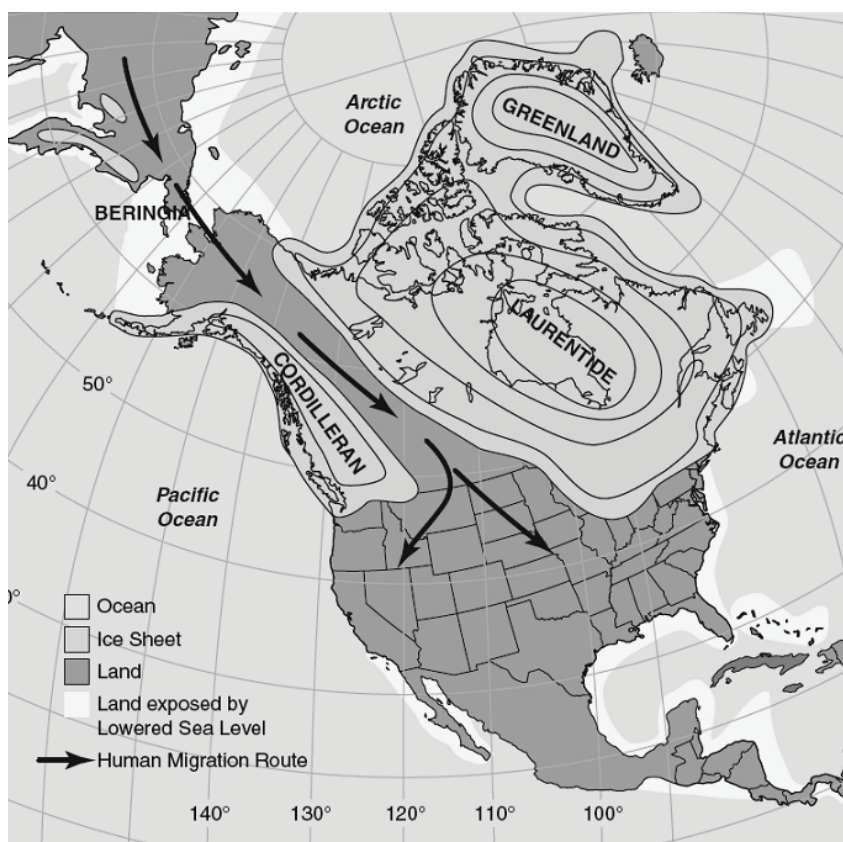


**Figure 1.** Continental configurations for various postulated times in the past: a) Rodinian supercontinent (late Precambrian) with a star identifying North America; b) Pleistocene (Ice Age) configuration; and c) modern configuration with arrows depicting post-Flood migration paths. (From Ross<sup>8</sup> figure 1.)





**Figure 2.** Map of sea levels at the Ice Age maximum showing the extent of the land surface



**Figure 3.** Map of the Bering seaway showing a possible pathway for animals and humans between the ice sheets (from Hartmann,<sup>25</sup> accessed 21 December 2015)

bridges would have facilitated animal migration after the Flood, allowing large mammals to reach the Americas and other continents. But how does this fit with the scattering of the people at the Tower of Babel? Does the timing coincide with the “division” of the earth that occurred during the days of Peleg as recorded in Genesis 10:25?

Morris has calculated from the biblical genealogies that Peleg was born about  $101 \pm 4$  years after the Flood.<sup>26</sup> And the Bible tells us Peleg lived 239 years (Genesis 11:18–19), giving a range of about 101–340 years after the Flood for the scattering of the nations at Babel. Snelling and Matthews believe the Babel event occurred on the low end of this time range, about 100 years after the Flood ended.<sup>13</sup> However, their timing was based primarily on an estimate that each generation was equivalent to about 30 years, not actual genealogical values listed in the text.<sup>13</sup>

Snelling and Matthews also estimated that the Ice Age proper

began about the same time as the Tower of Babel dispersion (100 years after the Flood) and ended just 250 years later at the approximate time Abraham was born, based on their ice accumulation calculations and interpretations of indirect evidence.<sup>13</sup> They consider the first 100 years after the Flood as a cooling period, when ice began to accumulate but had not yet reached sufficient levels to be designated as the Ice Age.<sup>27</sup> Part of the reason for their estimate is the lack of human tools and fossils found in pre-Ice Age sediments and radiocarbon dates of Ice Age fossils and radiocarbon dates found at the oldest human settlements.<sup>13</sup> From these data, they concluded that all settlements post-dated the Ice Age.<sup>13</sup>

Admittedly, there must have been a brief period right at the end of the Flood before the ice accumulated sufficiently to be designated as the Ice Age. But as the snow began to fall and ice began to build, high-latitude areas probably quickly began to be covered in ice, maybe within the first few decades, post-Flood. And if humans had not yet dispersed from the more moderate climates near Babel, as the Bible states, then it is no surprise that there is a lack of human fossils and/or artefacts in any pre-Ice Age sediments. Humans had not yet spread to these locations.

The estimate by Snelling and Matthews for the timing of the end of the Ice Age is more controversial.<sup>13</sup> A short, 250-year duration for the Ice Age seems less likely, based on the calculations by Oard<sup>24</sup> and the evidence for repeated ice advances and retreats observed across the northern continents.<sup>23</sup> The thicknesses of continental glacial depositional landforms (moraines, eskers, kames) also seem to suggest a much longer Ice Age that may have instead reached a glacial maximum 500 years post-Flood.<sup>24</sup>

Most cities initially sprang up in areas that were not glaciated, making direct observation of the timing of the post-Flood human settlements and the Ice Age sediments impossible. Snelling and Matthews were forced to rely on timing using radiocarbon dates instead.<sup>13</sup>

Because there is a lack of undisputed direct evidence for the end of the Ice Age, it seems reasonable to use the climate calculations by Oard as a model for making a timing estimation. This interpretation is possibly supported by the book of Job also. Henry Morris has pointed out that there are more references to snow and ice in the book of Job than in any other book of the Bible.<sup>28</sup> He admitted that the glaciers did not extend to the land of the Patriarchs, but it seems to have had a strong effect on the Middle Eastern climate, causing cooler temperatures and more rain and snow than witnessed there today, as reported in Job.<sup>28</sup> Without the Ice Age-induced climate effects in the Middle East, the area would probably have been warmer and more arid than what the book of Job seems to indicate.<sup>28</sup> Where does this lead us in terms of timing? Again, Henry Morris points out that the book of Job is likely the oldest book of the Bible, except

for possibly the first 11 chapters of Genesis.<sup>28</sup> Based on the lack of references in the Job text to Jewish law, the judges, the prophets, the nation of Israel, or Abraham, Morris placed the age of the book before Moses and possibly even before Abraham. He suggested we place the age of the book in the time of the Patriarchs, about 2000 BC.<sup>28</sup>

The interpretation in this paper differs from the timing estimated by Snelling and Matthews for the end of the Ice Age. But it is supported by the climate calculation estimates of Oard<sup>24</sup> and by the apparent cooler and wetter conditions that were still affecting the Middle Eastern climate during the time of the Patriarchs.<sup>28</sup> Exactly how long the ice sheets endured after their formation is unknown. They may have lasted an extra 500 years for a total duration of 1,000 years (figure 4). The land bridges, however, were directly dependent on the volume of ice (figures 2 and 3). As long as the ice remained, the land bridges also remained open for animal and human migration.

Finally, Oard has also calculated that the ice sheets formed during the Ice Age could rapidly melt away in less than 200 years as conditions changed.<sup>24</sup> Once the ice melted, the ocean water would immediately have risen, flooding the land bridges and coastal areas, effectively closing the opportunity for intercontinental migration (figure 1c).

### Man's disobedience

After the Flood, Nimrod encouraged mankind to remain in the Middle East area, "near a plain in the land of Shinar", building the Tower of Babel (Genesis 11:1–4). This was in direct disobedience to God's command to "be fruitful and multiply and fill the earth" (Genesis 9:1). It seems God divided and scattered the people by confounding their languages so that they would not miss the temporary, land bridge opportunity for migration (figure 4). If the Babel dispersion was closer to the end of Peleg's life, on the order of 250–340 years post-Flood, the ice would have had sufficient time to accumulate, lowering sea levels and providing sufficient land bridges between the continents in only a few additional generations after Babel (figure 4). A few generations may have been needed for humans to migrate to the Bering Sea land bridge from central Asia (figure 1c).

Because humans are capable of building ships, it should also be expected that some human populations crossed the ocean without the need for land bridges.<sup>29</sup> However, land animals (other than domestic) did not have this luxury and had to rely on land bridges to cross from one continent to the next. They were totally dependent on the timing of the Ice Age for access.

### Reason for the Ice Age

The Ice Age was an essential ending to the Flood event. Lowering sea levels and the creation of intercontinental land bridges seem necessary to provide migration pathways for large animals and humans. High ice volume was achieved at the same time migration pathways were needed to travel from the Middle East to distant continents now separated by water. The hotter ocean water likely kept the coastal areas warmer and ice-free for several centuries, providing a localised temperate climate, even while the Ice Age was nearing full force. After the oceans had cooled sufficiently and the volcanic activity began to wane, the ice sheets quickly melted and the land bridges disappeared beneath the rising ocean water, effectively ending the migration.

God provided the land bridges and removed the bridges via the Ice Age. The blatant disobedience of Nimrod was cause for God to confound the languages and force human migration before the migration opportunity was lost.

### Implications for the Flood/post-Flood boundary

This paper also has implications for the Flood/post-Flood boundary debate because it suggests that animals (and most humans) were only able to cross from continent to continent during the Ice Age, and not before. It is readily accepted that all Cenozoic rocks and fossils are pre-Ice Age. Therefore, advocates for a post-Flood boundary at, or fairly near, the Pliocene (just below the Ice Age) interpret the Cenozoic fossils as part of the latter stages of the Flood,<sup>2-7</sup> and possibly the receding water phase. They do not have to consider post-Flood migration pathways to explain the Cenozoic fossils.

Whereas, advocates for a K/T (or K/Pg) boundary for the end of the Flood consider all Cenozoic fossils to have

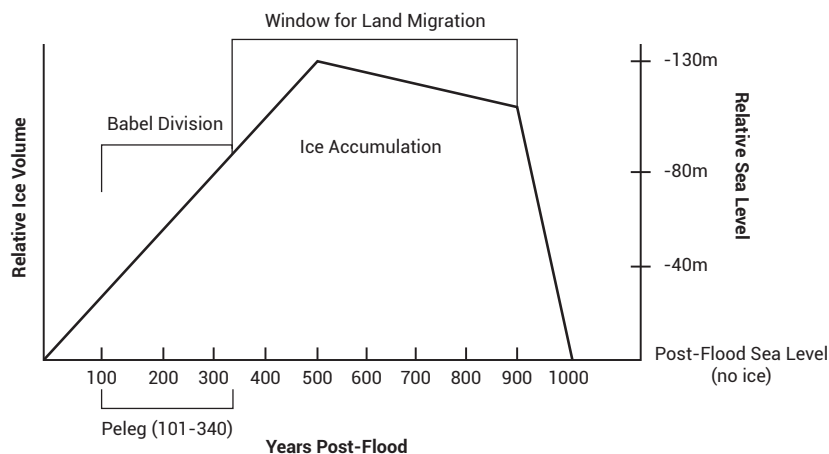
formed in the window of time between the ending of the Flood and the beginning of the Ice Age.<sup>1,8-12,14</sup> If Snelling and Matthews are correct,<sup>13</sup> this only allows about 100 years for the dispersal (whatever the mechanism) and incredible diversification and subsequent burial of all Cenozoic mammals, plants, and other fossils on multiple continents, and in nearly the exact same stratigraphic order, simultaneously. Therefore, the presumed 'local' catastrophes used to explain these Cenozoic fossils<sup>9-11</sup> seem to more closely resemble global catastrophes. And most global catastrophes are better explained with a global Flood event.

Advocates for a K/T post-Flood boundary must also explain how the Cenozoic animals, and in particular the large mammals, were able to migrate to the separated continents after the Flood without land bridges. As discussed previously, the suggestion of log mats may be viable for plants, insects, and small animals, but it is not very conducive for the larger animals. Land bridges seem to be necessary, but where did the land bridges come from, if not the Ice Age?

Ross, in particular, has championed the K/T boundary as the end of the Flood to explain the mammalian fossil record in North America. From his analysis, he has determined that nearly a quarter of pre-Flood mammal baramins in North America would have had to return again to North America after the Flood if the Flood/post-Flood boundary is chosen as the Pliocene/Pleistocene boundary.<sup>8</sup> He argued it is highly unlikely that such a high percentage of pre-Flood baramins would return to their pre-Flood locales, "display[ing] a proclivity to migrate to the graveyards of their deceased, pre-Flood baraminic kin".<sup>8</sup> Similarly, Ross also argued that the coincidence of kangaroo fossils found only in upper Cenozoic rocks in Australia and again found only living in Australia today, as additional support for a K/T or K/Pg post-Flood boundary.<sup>8</sup>

However, considering there are presently five habitable continental land masses, it is no surprise that about a quarter of the land animals returned to their pre-Flood locales after the Flood. They would have had about a one-in-five chance of returning to the same locations. A post-Flood 'sweepstakes' model of migration easily explains these probabilities.

And how can we be sure that kangaroos only migrated to Australia after the Flood? Maybe they did migrate elsewhere but have since died off in those other areas prior to the present. It is even possible that kangaroo fossils may have been buried elsewhere and have since eroded away



**Figure 4.** Timeline showing ice volume and sea level relationships vs years post-Flood, including an estimated 'window for land animal/human migration'. The ice accumulation curve is the same as the sea level curve due to their interdependency. As ice volume increases, the sea level drops in an inverse relationship. (Created by Mary Smith.)



or have not yet been exposed. Fossils and/or the lack of fossils may not reveal the whole story.

An unanswered question in Ross's analysis is just how were the post-Flood mammals able to return to their respective continents?<sup>8</sup> How did the kangaroos get to Australia after the Flood without land bridges providing the bulk of the pathway? Advocates of a K/T or K/Pg post-Flood boundary have not sufficiently considered the difficulties of post-Flood animal migration, particularly for the largest mammals and the hoofed animals.<sup>1,8,9,10,11,12,14</sup> Their suggestion that nearly all Cenozoic fossils were the result of post-Flood local catastrophes fails to explain how the post-Flood animals got to the various continents in the first place. They have not offered a testable, viable method for the migration of large animals to the newly separated continents after the Flood.

However, the Ice Age does provide a solution. Temporary land bridges, resulting from the formation of large continental ice sheets, provide an effective method for post-Flood animal and human migration. The Ice Age at the end of the Flood was no mere coincidence. It seems to have been an integral and necessary part of God's plan to disperse the animals and humans to the post-Flood continents.

## References

- Arment, C., Fossil snakes and the Flood boundary in North America, *J. Creation* **28**(3):13–15, 2014.
- Holt, R.D., Evidence for a Late Cainozoic Flood/post-Flood boundary, *J. Creation* **10**(1):128–167, 1996.
- Oard, M.J., Is the K/T the post-Flood boundary? Part 1: introduction and the scale of sedimentary rocks, *J. Creation* **24**(2):95–104, 2010.
- Oard, M.J., Is the K/T the post-Flood boundary? Part 2: paleoclimates and fossils, *J. Creation* **24**(3):87–93, 2010.
- Oard, M.J., Is the K/T the post-Flood boundary? Part 3: volcanism and plate tectonics, *J. Creation* **25**(1):57–62, 2011.
- Oard, M.J., Geology indicates the terrestrial Flood/post-Flood boundary is mostly in the Late Cenozoic, *J. Creation* **27**(1):119–127, 2013.
- Oard, M.J., Relating the Lava Creek ash to the post-Flood boundary, *J. Creation* **28**(1):104–113, 2014.
- Ross, M.R., Evaluating potential post-Flood boundaries with biostratigraphy—the Pliocene/Pleistocene boundary, *J. Creation* **26**(2):82–87, 2012.
- Whitmore, J.H. and Garner, P., Using suites of criteria to recognize pre-Flood, Flood, and post-Flood strata in the rock record with application to Wyoming (USA); in: Snelling, A.A. (Ed.), *Proceedings of the Sixth International Conference on Creationism*, Creation Science Fellowship and Institute for Creation Research, Pittsburgh, PA, and Dallas, TX, pp. 425–448, 2008.
- Whitmore, J.H. and Wise, K.P., Rapid and early post-Flood mammalian diversification evidence in the Green River Formation; in: Snelling, A.A. (Ed.), *Proceedings of the Sixth International Conference on Creationism*, Creation Science Fellowship and Institute for Creation Research, Pittsburgh, PA, and Dallas, TX, pp. 449–457, 2008.
- Snelling, A.A., *Earth's catastrophic past: Geology, Creation and the Flood*, Institute for Creation Research, Dallas, TX, 2009.
- Snelling, A.A., Geological issues; in: Boyd, S.W. and Snelling, A.A. (Eds.), *Grappling with the Chronology of the Genesis Flood*, Master Books, Green Forest, AR, pp. 77–110, 2014.
- Snelling, A.A. and Matthews, M., When Was the Ice Age in Biblical History? *Answers* **8**(2):44–52, 2013.
- Austin, S.A., Baumgardner, J.R., Humphreys, D.R., Snelling, A.A., Vardiman, L. and Wise, K.P., Catastrophic plate tectonics: a global Flood model of Earth history; in: Walsh, R.E. (Ed.), *Proceedings of the Third International Conference on Creationism*, Creation Science Fellowship, Pittsburgh, PA, pp. 609–621, 1994.
- Snelling, A.A., Geophysical issues; in: Boyd, S.W. and Snelling, A.A. (Eds.), *Grappling with the Chronology of the Genesis Flood*, Master Books, Green Forest, AR, pp. 111–144, 2014.
- Wise, K.P. and Croxton, M., Rafting: A post-Flood biogeographic dispersal mechanism; in: Ivey, R.L. (Ed.), *Proceedings of the Fifth International Conference on Creationism*, Creation Science Fellowship, Pittsburgh, PA, pp. 465–477, 2003.
- Statham, D., Natural rafts carried animals around the globe, *Creation* **33**(2): 54–55, 2011.
- Morris, J.D. and Austin, S.A., *Footprints in the Ash: The Explosive Story of Mount St. Helens*, Master Books, Green Forest, AR, p. 97, 2003.
- Oard, M.J., *The Genesis Flood and Floating Log Mats: Solving Geological Riddles*, Creation Book Publishers, Powder Springs, GA, 2014 (ebook).
- Vardiman, L., Tracking Those Incredible Hypercanes, *Acts & Facts* **41**(5): 12–14, 2012.
- Wood, T.C. and Murray, M.J., *Understanding the Pattern of Life: Origins and Organization of the Species*, Broadman & Holman Publishers, Nashville, TN, pp.187–203, 2003.
- Yoder, A.D. and Nowak, M.D., Has vicariance or dispersal been the predominant biogeographic force in Madagascar? Only time will tell, *Annual Review of Ecology, Evolution, and Systematics* **37**:423, 2006.
- Wicander, R. and Monroe, J.S., *Historical Geology: Evolution of Earth and life Through Time*, 7<sup>th</sup> edn, Brooks/Cole, Cengage Learning, Belmont, CA, 2013.
- Oard, M., *Frozen in Time: The Woolly Mammoth, the Ice Age, and the Bible*, Master Books, Green Forest, AK, 2004.
- Hartmann, D.L., Our changing climate: reports to the nation on our changing planet, [atmos.washington.edu/~dennis/OCC\\_Final\\_961216.html](http://atmos.washington.edu/~dennis/OCC_Final_961216.html), 17 December 1996 (accessed 21 December 2015).
- Morris, H.M., III, *The Book of Beginnings: A Practical Guide to Understand and Teach Genesis, Volume Two: Noah, the Flood, and the New World*, Institute for Creation Research, Dallas, TX, 2013.
- Personal communication, Andrew Snelling, 3 February 2016.
- Morris Jr, H.M., *The Remarkable Record of Job: The Ancient Wisdom, Scientific Accuracy, & Life—Changing Message of an Amazing Book*, Master Books, Green Forest, AR, 2000.
- Evenboer, T. and Terborg, P., The origin of American Indian populations, *J. Creation* **26**(1):71–75, 2012.

**Timothy L. Clarey** earned a Ph.D. and B.S. (summa cum laude) from Western Michigan University (USA), and a M.S. from University of Wyoming (USA) all in geology. He worked for nearly a decade as a geologist for a major oil company and then spent 17 years as a college professor. His publications include numerous articles on the geology of the Rocky Mountain region. He has written and/or co-authored four books, including *Guide to Dinosaurs (ICR)*. His latest Bible-based dinosaur book, published by Master Books, is entitled *Dinosaurs: Marvels of God's Design*. Tim currently works as a Research Associate for Institute for Creation Research in Dallas.

# Promoter evolution is impossible by random mutations

Jean O'Micks

According to a change in evolutionary paradigms, mutations in the regulatory circuitry of genes has been suggested as the major force behind morphological changes during evolution. Even though we cannot observe mutations going on in the regulatory region of genes one by one, these events can still be modelled *in silico* via computer programs, such as PromMute. This program simulates point mutations happening over a set number of generations within a promoter sequence. PromMute models the formation of several target transcription factor binding sites from random sequences. This paper examines how successfully target regulatory modules can form via random mutations with increasing numbers of motifs, which can also be constrained by physical distance as modelled by PromMute. The results indicate that longer and larger numbers of motifs make it more and more difficult, virtually impossible, for regulatory modules to form by random mutation, as required by molecular evolution, especially so with added spatial constraints.

Previous creationist publications have detailed how genetic conservation is not capable of driving molecular evolution. This is because evolution demands the flux of newly generated genetic elements over the course of evolutionary time. Thus, 'evolutionary conservation' is an oxymoron, in that change cannot be affected by conservation and stasis.<sup>1</sup>

Ohno<sup>2</sup> recognized this and realized that instead of newly evolving genes, changes behind the regulation of existing genes are responsible for changes in phenotype, thereby supposedly affecting evolutionary development. This has become a new paradigm within molecular evolution.<sup>3</sup> For example, it is thought that different variants, differing by 1 bp of the palindromic P3 motif TAATYNRATTA reside in the regulatory region of the rhodopsin gene in subsets of *Drosophila* photoreceptors.<sup>4</sup>

The question arises, besides the coding regions of genes, how did the regulatory region of genes arise via random mutations? It is one thing to explain how genes arise via random mutations, which isn't much dealt with, but it is another thing to explain how a functioning regulatory region arises by random mutations. Furthermore, both gene regions have to be present in order for a gene to function properly. An assembly line can have all the necessary mechanical parts in place, but if there is no process which turns on the assembly line and modulates its function, then the assembly line achieves nothing.

The regulatory region of a gene is a complex genetic structure, which includes the promoter, which is that part of the genome just upstream of a given gene, as well as enhancer elements, and the first introns of the gene. Distal enhancers also take part in gene regulation which may even reside on other chromosomes. In general, the promoter

can be delineated as the section of the gene -500 to +100 bp around the transcription start site (TSS). Some authors define the promoter length as 1,000 to even 3,000 or 5,000 bp. The promoter is a stretch of DNA which contains so-called transcription factor binding sites (TFBSs), also known as regulatory motifs (or just simply motifs in the rest of this paper). These motifs are the docking sites of transcription factors (TFs), generally proteins, which bind with their surface to the face of the TFBS in a lock and key manner. Motifs are generally between 5–20 bp long, and are characterized by a more or less definitive sequence. Physico-chemical interactions between amino acid side chains on the TF surface and the bases in the DNA are integrated so as to affect gene regulation. Some TFs induce gene expression, some act as repressors. Depending on how the TF binds to its motif, some positions within the motif sequence can be degenerate. For example, the sequence for the ABRE element ACGTGKC is degenerate at position six, where K = G/T. Motifs can also form regulatory modules, where multiple motifs and TFs act in concert to modulate the behaviour of Polymerase II, which initiates gene transcription.<sup>5</sup>

Since motif sequences are relatively short compared to the sequences of whole genes, it would be interesting to examine how motifs could have come into existence via random genetic mutations. Motifs could form via series of single base pair mutations. However, it is impossible to follow single base pair mutations within a population of organisms over hundreds or thousands of generations during evolutionary time, which are needed for the motifs themselves to form. The best we can do to approximately model this process is to simulate promoter evolution *in silico*.

## Results

Several candidate promoter mutation simulation programs were examined to use in this analysis, such as *ev*,<sup>6</sup> *PPE*,<sup>7</sup> and *PromMute*.<sup>8</sup> The program *PromMute* was chosen due to several considerations: as opposed to *ev* and *PPE*, *PromMute* simulated a wider variety of real motifs in a longer promoter segment 1 Kbp long. Position weight matrixes (PWMs) were used to score possible occurrences of target motifs. A PWM is a 4xn matrix, which represents a motif n bp long, and is used to score the occurrence of a motif. Each of the positions of the motif's occurrence is scored based on which of the 4 bases (A, C, G, or T) they match. All positional subscores are added up to give the score for the occurrence of a given motif.

Motifs were simulated to form anywhere within the promoter region. Most importantly, as opposed to *ev* and *PPE*, *PromMute* doesn't allow for the selection of partially formed motifs. This is because natural selection cannot operate on a partially present motif, because a motif either functions, or it doesn't—it either binds its corresponding TF or it doesn't. This follows binary logic. In this respect, regulatory motif modules are irreducibly complex systems. In order for a valid promoter region to evolve in the *PromMute* program, all target motifs have to be fully functional (with a score of its occurrence at least 90% of the maximum score of its corresponding PWM). In other words, all target motifs have to have undergone a gain of function mutation, resulting in the motif being newly capable of binding its TF. *PPE* uses real promoters in its simulation, whereas *PromMute* uses a random sequence, but this is actually ideal to simulate the appearance of islands of meaningful genetic signals in a sea of random, meaningless sequence.

### Description of the PromMute program

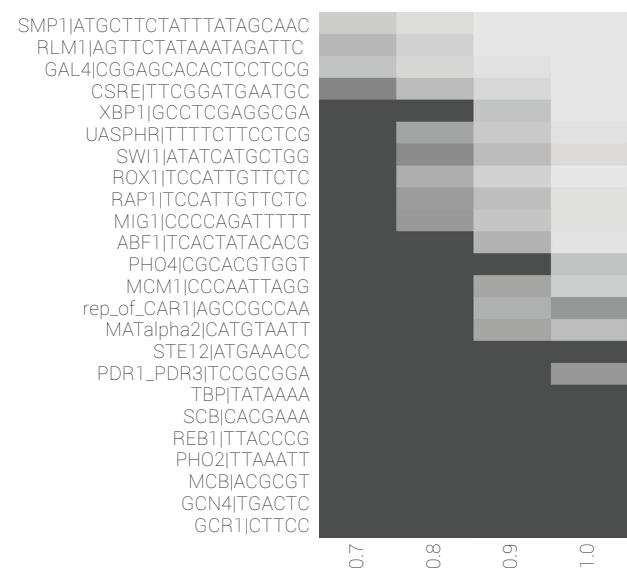
*PromMute* simulates point mutations in a promoter of a set size within a set number of organisms over a set number of cycles/generations. In each promoter, the optimal occurrence of each motif is determined in each organism (that is, the closest to the target motif sequence which is the highest-scoring occurrence). Each motif occurrence is scored according to its PWM, and if the ratio of its score divided by the maximum score of that PWM is above the motif cut-off limit, then that occurrence of that motif is deemed functional. The lowest scoring organisms (bottom 50%) are eliminated and their place is taken over by organisms from the top 50% by binary division (this simulates natural selection). All of this happens in one generation, and the goal is to reach a point where all selected target motifs become functional. If all motifs are functional except one, the simulation keeps on running. Either all motifs become

functional eventually or the simulation halts after the set number of cycles.

*PromMute* was run five times with sets of one, two, or three motifs, and the average number of generations were taken to describe the amount of time needed for these motif(s) to form. If the program ran for 10,000 generations, it was assumed that the motif(s) weren't able to form. A selection cut-off of 0.5 was chosen, and motif cut-offs of 0.7, 0.8, 0.9, and 1.0 were analyzed for 100 organisms for single motifs, and a motif cut-off of 0.9 for motif pairs and triplets. *PromMute* was also developed so as to halt when all target motifs were formed within a specified spacer region of 100 bp. This was done for the analysis of motif pairs and triplets. In this analysis a motif is synonymous with a transcription factor binding site (TFBS). In total five sets of analyses were run: single TFBS, pairs of TFBS with and without spacers, and TFBS triplets with and without spacers.

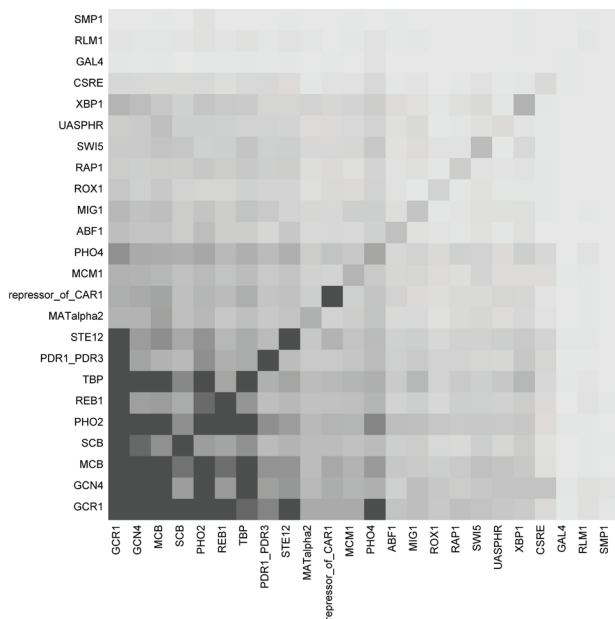
### Single motifs

All 24 motifs from the Promoter Database of *Saccharomyces cerevisiae* (SCPD) were analyzed, and the log10 value of the number of generations needed for each motif to form is depicted in figure 1 for motif cut-off values of 0.7–1.0. Black denotes a log10 value of zero (one generation), whereas light grey denotes a log10 value of four (10,000 generations). We can see that the longer a motif is, and the higher the motif cut-off is, the longer it takes for a



**Figure 1.** Log10 values of generation times needed for the 24 regulatory motifs to form individually in a proximal promoter as simulated by *PromMute* for motif cut-off values of 0.7, 0.8, 0.9, and 1.0. Black values correspond to a generation of 1, or a log10 generation time of 0. Light grey values correspond to log10 values of 4, corresponding to 10,000 generations.





**Figure 2.** Heat map of log<sub>10</sub> generation time for the formation of pairs of motifs. Black values correspond to a generation of 1, or a log<sub>10</sub> generation time of 0. Light grey values correspond to log<sub>10</sub> values of 4, corresponding to 10,000 generations.

given motif to form. At smaller lengths of 5–8 bp for motifs such as GCR1 (CTTCC) and GCN4 (TGACTC) we can see that these motifs form within short periods of time. This is not surprising, since a motif 5 bp long occurs randomly once every  $4^5 = 1,024$  bp, which is very close to the size of the proximal promoter that was simulated.

Motifs of length 13 bp and longer do not form by chance at a motif cut-off of 1.0, whereas motifs of length 18–20 bp do not form at a motif cut-off of 0.9–1.0 according to the settings of the PromMute program.

The average log<sub>10</sub> generation value (where the generation value was not assumed to be unlimited) is 1.43 for a motif cut-off of 0.9.

## Motif pairs

The formation of motif pairs was examined at a motif cut-off value of 0.9. Here  $24 \times 24 = 576$  possible pairs were studied. As we can see in figure 2, darker shades correspond to log<sub>10</sub> values of 0 (one single generation), whereas lighter shades correspond to values of 4 (10,000 generations). As we can see, motif pairs each under 10 bp (such as PHO4) in length had no serious difficulty forming. The longer motifs, such as GAL4 (17 bp), RLM1 (18 bp), and SMP1 (20 bp) all showed log<sub>10</sub> values of close to four (10,000 generations) when paired up with all other motifs.

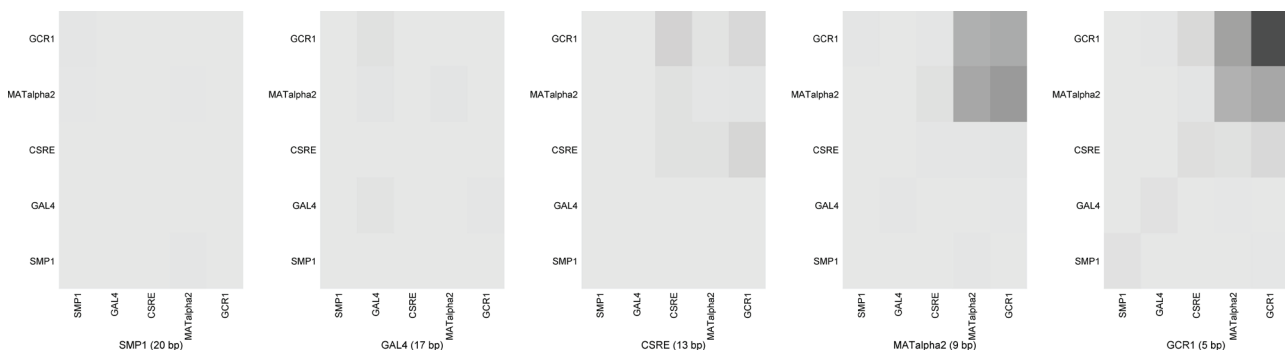
## Motif triplets

Because of spatial restraints in depicting the results for 13,824 triplet motifs stemming from 24 motifs, five motifs were chosen: GCR1, a very short motif (5 bp); MATalpha2, a short motif (9 bp); CSRE, an average length motif (13 bp); GAL4, a long motif (17 bp); and SMP1, a very long motif (20 bp), each 4 bp longer than the previous motif. This way we can see how motifs of different lengths behave when put together in triplets.

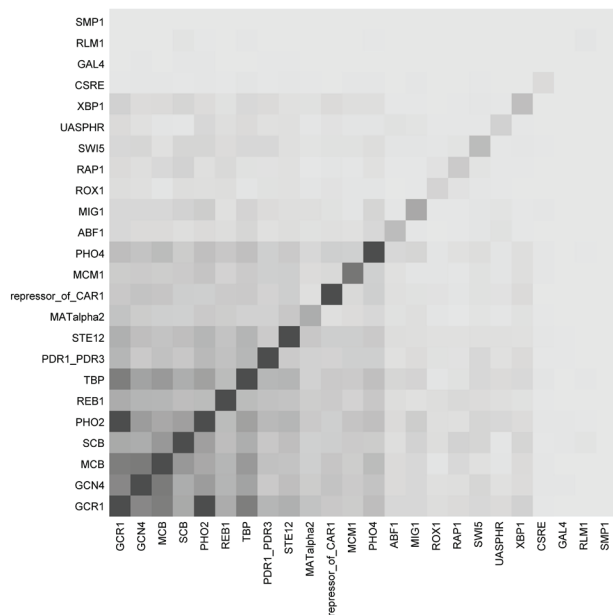
As we can see, the generation time for each triplet-based module has greatly increased (figure 3). The average log<sub>10</sub> generation value rose from 2.8 for motif pairs to 3.56 for motif triplets. The difference is 0.75, meaning that it is  $10^{(3.56-2.8)} = 10^{0.76} = 5.75$  times more difficult for motif triplets to form than motif pairs. This is the degree of difficulty which arises when one more motif is added for random mutations to form.

## Motif combinations with spacer restrictions

The PromMute program was further developed in that it took certain spacer restraints into consideration, since TFs act in concert to influence gene expression. Lu *et al.*<sup>9</sup> demonstrated the distance conservation of transcription regulatory motifs in human promoters. For example, the



**Figure 3.** Heat map of log<sub>10</sub> generation time for the formation of motif triplets. Black values correspond to a generation of 1, or a log<sub>10</sub> generation time of 0. Light grey values correspond to log<sub>10</sub> values of 4, corresponding to 10,000 generations.



**Figure 4.** Heat map of log10 generation time for the formation of pairs of motifs constrained by a spacer motif of 100 bp. Black values correspond to a generation of 1, or a log10 generation time of 0. Light grey values correspond to log10 values of 4, corresponding to 10,000 generations.

*E1B* adenovirus gene diminishes in activity, if the spacing increases between the GC-box and the TATA-box.<sup>10</sup> In order to do this, TFs must also be in each other's spatial vicinity. Thus the motifs themselves must be relatively close to each other in order for their corresponding TFs to dock to each other.

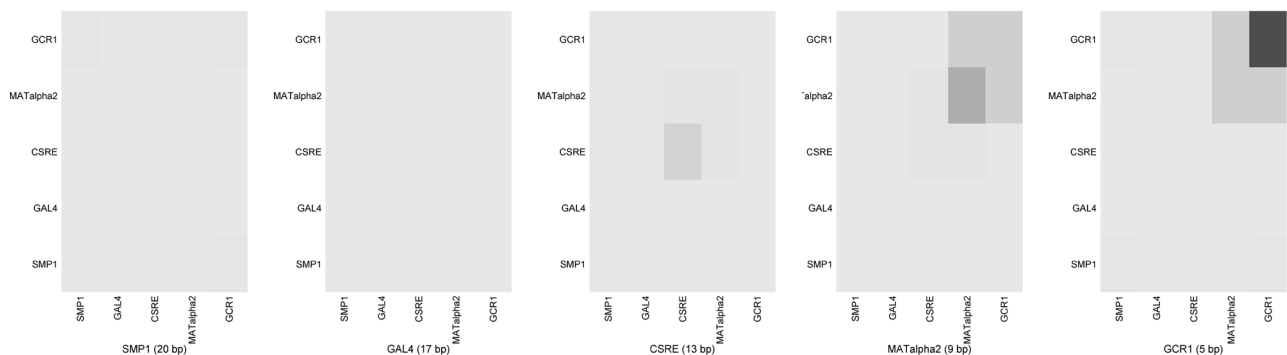
A total 25,976 human proximal promoters 1 Kbp long were downloaded from the Swiss Institute of Bioinformatics, and 127 human PWMs were downloaded from the JASPAR database. All 127 PWMs were scanned in each of the human proximal promoters at a motif cut-off value of 0.9. The average distance between two motifs was found to be 110 bp, but this was approximated in this study with a spacer of 100 bp.

Figure 4 shows the log10 values of the generation number needed for the formation of motif pairs within the spacer limit. As we can see, on a global level, log10 generation values have shifted to higher values as the effect of the spatial constraint of requiring both motifs to be found within 100 bp of each other. Compared to motif pairs without the spacer restraint the average log10 generation values (where the generation value was not assumed to be unlimited) is 3.3 for motif pairs with spacer, and 2.8 without. The difference is 0.5, meaning that it is  $10^{(3.3-2.8)} = 10^{0.5} = 3.2$  times more difficult for motif pairs to form with a spacer requirement than pairs unbound by this limitation requirement.

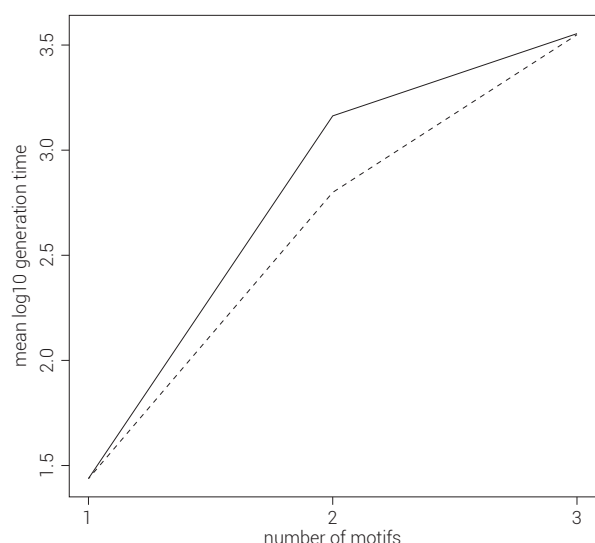
When motif triplets were analyzed with spacers (see figure 5), the average log10 generation value rose from 3.2 to 3.6. Thus it is  $10^{(3.6-3.2)} = 10^{0.4} = 2.5$  times more difficult for spaced motif triplets to form than spaced motif pairs. When adding spacers to motif triplets, it is only  $10^{(3.6-3.56)} = 10^{0.04} = 1.1$  times more difficult for this kind of regulatory module to form when just considering motif triplets. Figure 6 shows the relationship between the average log10 generation values for single motifs, motif pairs, and motif triplets with and without spacers.

## Discussion

We can draw a number of interesting conclusions from this analysis of the *in silico* simulation of motifs in promoter sequences. First of all, it validates the concept of disallowing the selection of partially formed motifs. As illustrated in the original paper, the longer a motif is, the larger surface it exposes to random mutations which can fragment it. If we take a run to be a number of consecutive generations, with its own unique PWM score, then this increased rate of motif fragmentation results in a larger number of runs of shorter lengths. If you have a short motif, then it will hardly be interrupted by any mutations, and its PWM score stays the same for a long time. However, a longer motif fragments more easily, and thus the PWM fluctuates a lot. This means the chances are higher that a random mutation occurs within



**Figure 5.** Heat map of log10 generation time for the formation of motif triplets constrained by a spacer motif of 100 bp. Black values correspond to a generation of 1, or a log10 generation time of 0. Light grey values correspond to log10 values of 4, corresponding to 10,000 generations.



**Figure 6.** Mean log10 generation time for single motifs, pairs of motifs, and motif triplets with spacer constraint (solid curve), and without such constraint (dashed curve)

the motif, thereby destabilizing it or even causing a loss of function mutation, or lowering its PWM score. Thus, a random mutation can take the motif either closer to its functional, target sequence, but it can also step away from it.

Mathematically speaking, this problem is similar to the random walk of a drunken sailor. Starting from a random motif sequence, the individual positions of the motif must all consecutively mutate to the correct base. This corresponds to a random walk of the drunken sailor stumbling consecutively in one direction (towards build-up of the target sequence). Longer sets of steps going consecutively in one direction are less and less likely.

The whole goal of the PromMute simulation is to demonstrate whether target motifs with a defined sequence can arise via a series of random mutations, called a ‘mutational trajectory’. Such a trajectory is depicted in figure 7, namely T,T,T,T,C,T,T,C,C,A,G,C which transforms the random motif GAGGCCTCAACA into the target

12 - TCCATTGTTCTC  
 11 - TCGATTGTTCTC  
 10 - TCGATTTTCTC  
 9 - TCGGTTTTCTC  
 8 - TCGGTTTTCTA  
 7 - TCGGTTTTCTA  
 6 - GCGGTTTTTATA  
 5 - GCGGTTTAAATA  
 4 - GAGGTTTAAATA  
 3 - GAGGTTTAAACA  
 2 - GAGGCTTCAACA  
 1 - GAGGCTTCAACA  
 0 - GAGGCCTCAACA

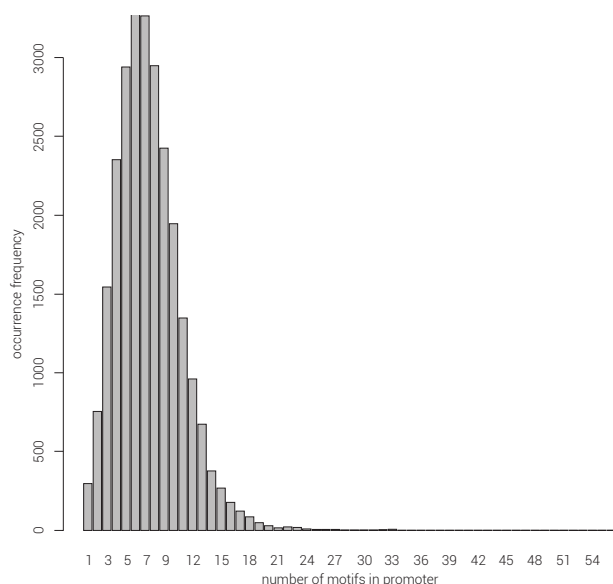
**Figure 7.** Formation of target motif according to drunken sailor random walk model. Here 3 bp of a random 12-mer may match the target motif sequence at the top by random chance. At a motif cut-off of 0.9, 11 – 3 = 8 bp need to match with at least 90% of the positions of the target sequence. This means that eight consecutive mutations have to occur to match the target, which has a probability of  $10^{-0.325 \times 12} \sim 10^{-4}$ .

motif TCCATTGTTCTC. If we have a random motif of length  $n$  bp,  $n/4$  bp of this random motif will match the sequence of the target motif without any mutations having happened. If we select a motif cut-off of 0.9, this means that the initial random motif must follow a mutational trajectory, whereby 90% of its bases will match the sequence of the target motif. This corresponds to  $(0.9 - 0.25)n = 0.65n$  mutations happening in the right order for this to happen. In figure 7, this means equals  $0.65 \times 12 \sim 8$  mutations for a motif of length 12. This is similar to the Hamming distance concept of how different two sequences are. At each step along the trajectory, a single nucleotide at a given position has a 1/3 chance of mutating to the proper base. Since the nucleotide is changing, it has to mutate to the correct bp of the remaining three possibilities other than itself, if theoretically, all possible bp mutations have the same probability. This probability is equal to  $3^{-0.65n}$ , which is approximately  $10^{-0.325n}$ . For a motif of length 12, this probability is approximately  $10^{-4}$ . If a module of five motifs, each of length 12, is required to form a regulatory module within a promoter, the chance for this to happen at random is  $10^{-20}$ . This probability has been defined by evolutionist Richard Dawkins<sup>11</sup> as low enough for an event to be practically impossible.

Based on previous analyses, on average, 7.41 motifs were found in each promoter with a range between 1 and 56, a median of 7, and a standard deviation of 3.38. The distribution of the frequency of motifs per proximal promoter can be seen in figure 8. As we can see, it follows a normal distribution with a slight skew to the right. Forming a proximal promoter with seven motifs is hard enough, but one with 56 motifs surely must be insurmountable for molecular evolution to achieve. However, even if this promoter contains redundant regulatory modules, the formation of seven motifs at once is approximately  $10^{-28}$ . As a test, PromMute was run with a spacer value of 100 bp to simulate a real promoter with seven motifs: GCR1 (5bp), MCM1 (10 bp), ABF1 (12 bp), MIG1 (12 bp), CSRE (13 bp), GAL4 (17 bp), and SMP1 (20 bp) as a realistic test. Five runs showed that the TFBS complex could not form.

When studying motif pairs it was observed that the longer motifs, such as GAL4, RLM1, and SMP1, all showed log10 values of about 4





**Figure 8.** Occurrence frequency of given number of motifs in human proximal promoters (1 Kbp)

(10,000 generations). Since in figure 1 these same motifs also showed log10 values of four, these motifs masked out the effect that any shorter motif might have besides it. This is not surprising, since it is harder for another motif to form if in and of itself a longer motif doesn't form by random chance. Decreases in average log10 generation values after addition motifs is expected to taper off and reach a plateau. This is because it is more and more difficult for additional motifs to form by chance.

We must further note here that besides simulating a select number of target motifs in a hypothetical promoter, we still have not modelled fully realistic motifs. Whereas the formulation of triplet motifs is albeit hard, but still possibly feasible in some cases with shorter motifs, many promoters contain modules of more than three motifs. Based on calculations using 1 Kbp human promoters and PWMs, it was found that there are 7.41 motifs in a given human promoter on average. Since all human motifs are not known, this number could be even higher.

Also, we must take into consideration, that the mutation rate used in PromMute was  $10^{-3}$ , which is three to five times higher than the average mutation rate in nature. Therefore generation times needed for the formation of motifs/modules should be multiplied by 1,000.

### Tandem repeats, CpG islands, G-quadruplexes

Gene regulation does not occur exclusively by TFBS. Other regulatory elements include short tandem repeats (STR), G-quadruplexes (G4), and CpG islands (CGI), which all affect gene regulation in their own special way.

STRs are repeats of short stretches of DNA 2–5 bp long. About 17% of human genes and 25% of yeast genes have at least one STR in their regulatory elements.<sup>12,13</sup> STRs generally do not overlap with TFBS. For example, the number of CAG repeats in exon 1 of the SK3 calcium-activated potassium channel influences the severity of schizophrenic symptoms.<sup>14</sup>

G-quadruplexes are guanine-rich tracts where four or more tandem guanine tracts can fold into a four-stranded secondary structure, induced by transcriptional perturbation. G4s can hinder the translocation of helicase and thus cause transcription arrest.<sup>15</sup> CGIs determine the number of PolII binding sites, and promoters with CGIs are characterized by high transcriptional activity.<sup>16</sup>

Besides distance constraints between pairs of motifs, several regulatory motifs are constrained as to how far away they are from the TSS, based on a study of the distribution of 165 TRANSFAC motifs in 600 bp human promoters. Not only this, but motif pairs also show functional association.<sup>17</sup> This is because the TFs which bind to these TFBSs interact with the PolII protein during transcription.

### Summary and conclusion

According to a shift in evolutionary paradigms, and also as pointed out in the creationist literature, molecular evolution has a lot to overcome in explaining how the coding regions of genes evolved, but also as to how their regulation also evolved. As two halves of a whole, both the coding region and its promoter are fundamentally necessary to form and start functioning at exactly the same time. All this is needed for hundreds of genes in order for a minimal organism to be viable.<sup>18</sup>

Statistically speaking, a shorter motif has a higher chance of being present in a long enough stretch of sequence. For example, there are  $4^5 = 1,024$  different kinds of pentamers. A pentamer of any sequence is expected to occur every 1,000 bp, which is the length of the promoter region in the analysis. A 10-mer occurs once every  $4^{10} = 1$  Mbp. Therefore random mutation-based evolution would have to work very hard to form such a target 10-mer out of a random stretch of sequence. If random mutations have to form a whole number of motifs, and which also must fall within a certain distance from one another, all these additional complicating circumstances make it even more impossible for molecular evolution to form a regulatory module out of nothing (especially when taking spatial constraints into consideration). If position from the TSS would also be taken into consideration as an added realistic factor, then this hurdle would increase even more.

Multiple TFBSs form a complex module in order to regulate gene expression, with all of them needed to be present at one time and in the same place. Natural selection acts upon fully formed regulatory modules as a whole,

**Table 1.** Motif name, sequence, and maximum PWM value of the 24 yeast regulatory motifs in the SCPD

Motif	Sequence	Motif length	Maximum PWM score
GCR1	CTTCC	5	7.711
GCN4	TGACTC	6	9.482
MCB	ACGCGT	6	9.783
PHO2	TTAAATT	7	9.542
REB1	TTACCCG	7	11.511
SCB	CACGAAA	7	11.323
TBP	TATAAAA	7	10.663
PDR1/PDR3	TCCGCGGA	8	13.546
STE12	ATGAAACC	8	11.469
MATalpha2	CATGTAATT	9	14.137
repressor_of_CAR1	AGCCGCCAA	9	12.798
MCM1	CCCAATTAGG	10	13.914
PHO4	CGCACGTGGT	10	12.144
ABF1	TCACTATACACG	12	14.804
MIG1	CCCCAGATTTTT	12	15.148
RAP1	ACACCACATACAC	12	15.91
ROX1	TCCATTGTTCTC	12	16.124
SWI5	ATATCATGCTGG	12	13.796
UASPHR	TTTTCTTCTCG	12	14.823
XBP1	GCCTCGAGGCGA	12	15.052
CSRE	TTCGGATGAATGG	13	16.731
GAL4	CGGAGCACACTCCTCCG	17	19.931
RLM1	AGTTCTATAAATAGATTC	18	22.37
SMP1	ATGCTTCTATTTATAG-CAAC	20	24.945

and not on partial motifs. The formation of functional, information-bearing genetic elements does not happen by random genetic mutations; rather they are design elements which have been specifically created to work together to regulate the gene that they reside in.

### Materials and methods

The Windows program PromMute, as described in Cserhati 2012,<sup>8</sup> was rewritten in perl so that a user can run it at a Linux command prompt. A list of one or more target regulatory motifs from the *Saccharomyces cerevisiae* Promoter Database (SCPD)<sup>9</sup> can be supplied as a parameter of the simulation. These motifs are listed in table 1.

Heat maps were created using R version 3.2.4.

1 Kbp human promoters (–1,000 to –1 bp) were downloaded from the Swiss Institute of Bioinformatics ([www.isb-sib.ch/](http://www.isb-sib.ch/)). PWMs for human TFBSs were downloaded from the JASPAR database<sup>20</sup> ([jaspar.genereg.net/](http://jaspar.genereg.net/)).

Perl scripts and matrixes are available at the following URL at GitHub: [github.com/jeanomicks/prommute\\_scripts](https://github.com/jeanomicks/prommute_scripts).

### References

- Cserhati, M., Creation aspects of conserved non-coding sequences, *J. Creation* **21**(2):101–108, 2007.
- Ohno, S., *Evolution by Gene Duplication*, Springer-Verlag, Heidelberg, Germany, 1970.
- Carroll, S.B., Endless forms: the evolution of gene regulation and morphological diversity, *Cell* **101**(6):577–580, 2000.
- Rister, J., Razzaq, A., Boodram, P. *et al.*, Single-base pair differences in a shared motif determine differential Rhodopsin expression, *Science* **350**(6265): 1258–1261, 2015.
- Wray, G.A., Hahn, M.W., Abouheif, E. *et al.*, The Evolution of Transcriptional Regulation in Eukaryotes, *Mol. Biol. Evol.* **20**:1377–1419, 2003.
- Schneider, T.D., Evolution of biological information, *Nucleic Acids Res.* **28**: 2794–2799, 2000.
- Stone, J.R. and Wray, G.A., Rapid evolution of cis-regulatory sequences via local point mutations, *Mol. Biol. Evol.* **18**:1764–1770, 2001.
- Cserhati, M., PromMute—A Promoter Mutation Simulation for Modeling the Evolution of Genetic Regulatory Elements, *J. Comput. Sci. Syst. Biol.* **5**: 074–080, 2012.
- Lu, J., Luo, L. and Zhang, Y., Distance conservation of transcription regulatory motifs in human promoters, *Comput. Biol. Chem.* **32**(6):433–437, 2008.
- Grace, M.L., Chandrasekharan, M.B., Hall, T.C. *et al.*, Sequence and spacing of TATA box elements are critical for accurate initiation from the beta-phaseolin promoter, *J. Biol. Chem.* **279**(9):8102–8110, 2004.
- Dawkins, R., *The Blind Watchmaker: Why the Evidence of Evolution Reveals a Universe Without Design*, W.W. Norton, New York, 1996.
- Bolton, K.A., Ross, J.P., Grice, D.M. *et al.*, STARRRT: a table of short tandem repeats in regulatory regions of the human genome, *BMC Genomics* **15**:14:795, 2013.
- Abe, H. and Gemmell, N.J., Abundance, arrangement, and function of sequence motifs in the chicken promoters, *BMC Genomics* **15**:15:900, 2014.
- Grube, S., Gerchen, M.F., Adamcio, B. *et al.*, CAG repeat polymorphism of KCNN3 predicts SK3 channel function and cognitive performance in schizophrenia, *EMBO Mol. Med.* **3**(6):309–319, 2011.
- Zhang, C., Liu, H.H., Zheng, K.W. *et al.*, G-quadruplex formation in response to remote downstream transcription activity: long-range sensing and signal transducing in DNA double helix, *Nucleic Acids Res.* **41**(14):7144–7152, 2013.
- Elango, N. and Yi, S.V., Functional relevance of CpG island length for regulation of gene expression, *Genetics* **187**(4):1077–1083, 2011.
- Vardhanabhuti, S., Wang, J. and Hannenhalli, S., Position and distance specificity are important determinants of cis-regulatory motifs in addition to evolutionary conservation, *Nucleic Acids Res.* **35**(10):3203–3213, 2007.
- O'Micks, J., Bacterial genome decay from a baraminological viewpoint, *J. Creation* **29**(2):110–118, 2015.
- Zhu, J. and Zhang, M.Q., SCPD: a promoter database of the yeast *Saccharomyces cerevisiae*, *Bioinformatics* **15**:607–611, 1999.
- Mathelier, A., Zhao, X., Zhang, A.W. *et al.*, JASPAR 2014: an extensively expanded and updated open-access database of transcription factor binding profiles, *Nucleic Acids Res.* **42**(Database issue):D142–147, 2014.

**Jean O'Micks** has a Ph.D. in biology. He has been an active creationist for 15 years and takes a great interest in molecular biology. He has published a number of articles in Journal of Creation.

# Flood processes into the late Cenozoic—sedimentary rock evidence

Michael J. Oard

This paper summarizes seven general features of most Cenozoic sedimentary rocks best explained by Flood processes. These are the sometimes great thicknesses; sometimes widespread, relatively thin layers; sediment lithification; widespread and/or thick 'evaporites'; phosphorites; carbonates; and thick continental margin rocks.

Recently, John Whitmore has defended the thesis that post-Flood mass wasting processes have the potential to explain the majority of the Cenozoic rock record, thus justifying the placement of the Flood/post-Flood boundary at or near the Cretaceous/Tertiary (K/T) boundary.<sup>1</sup> This defence extends his previous articles on the subject from the 2008 International Conference on Creationism.<sup>2,3</sup> Whitmore has also done research on the Green River Formation, dated as early Cenozoic and the subject of his Ph.D. thesis, and participated in a forum with me on whether the Green River Formation is Flood or post-Flood in the *Journal of Creation* issue 20(1) in 2006.<sup>4</sup> Although there are problems with both interpretations, Whitmore believes the Green River Formation is the product of post-Flood lakes,<sup>5</sup> while I believe it is a Flood deposit.<sup>6</sup>

Whitmore argues that post-Flood mass wasting of generally unlithified sediments during mountain uplift, heavy precipitation, a lack of vegetation, giant earthquakes, meteorite impacts, and massive volcanic activity can explain the geology, paleontology, and geomorphology deduced from believing the Cenozoic is post-Flood. Mass wasting or mass movement refers to all the processes by which soil and rock are eroded and transported downslope by gravity.<sup>7</sup> It includes slow displacements such as creep and rapid movements such as rockfalls, rockslides, and debris flows. Although Whitmore's scenario for post-Flood catastrophism seems plausible, there are numerous problems. Mass wasting occurs today and would have been more intense early in the post-Flood period, but it is the *magnitude* of these features, deduced from the Cenozoic, that is the main problem. Thousands of metres of mountain uplift and basin sinking, and thousands of metres of erosion and deposition occurred in the Cenozoic, which Whitmore acknowledges and places *after* the Flood:

"In short these processes should have either taken off hundreds to thousands of meters of sediments from that surface or buried that surface with hundreds to thousands of meters of sediments."<sup>1</sup>

Furthermore, the scenario fails to explain the unique geomorphological features left on the earth's surface after erosion. This series of articles will elaborate on many features prevalent in the Cenozoic rock record, which often extend into the very late Cenozoic, that are better explained by Flood processes than post-Flood catastrophism,<sup>8</sup> starting with sedimentology in this part (table 1). In the final paper, I will address Whitmore's major arguments in more detail.

## Huge volume of Cenozoic sedimentary rocks

It has been claimed that the Cenozoic erathem is post-Flood because it has less sedimentary extent than the Mesozoic and Paleozoic erathems.<sup>9</sup> However, the volume of Cenozoic rocks in the world is still sufficiently large to make this a poor argument for locating the end of the Flood.<sup>10,11</sup> Besides, even those who place the post-Flood boundary in the late Cenozoic expect less global and more local and regional sedimentation to have occurred later in the Flood. And ironically, if we compare erathems, the collective Cenozoic erathem, based on data from secular geologists, actually contains a larger volume of sedimentary rocks than any of the other nine Phanerozoic systems (figure 1).<sup>11</sup>

It is not only the huge volume of Cenozoic rocks that challenge post-Flood explanations of much of the Cenozoic but also the thickness of Cenozoic sedimentary rocks at individual locations. Thickness is a subjective term, but the thickness magnitudes are in some cases beyond comprehension—for a post-Flood scenario. Cenozoic deposits can be very thick in basins and very widespread on plains near uplifts.<sup>6</sup> Many basins around the world contain thousands of metres of Cenozoic sedimentary rocks. Whitmore mentions 10,000 m of Cenozoic sedimentary rocks in the large valley of south-east California,<sup>1</sup> but 6,000 m of this is *late Cenozoic*.<sup>12</sup> He believes these sediments must be deposited after the Flood. Other basins in southern California have just as much Cenozoic sedimentary rocks. The Los Angeles, California, basin subsided in the late Cenozoic collecting about 6,000 m of sediment, now



sedimentary rock.<sup>13</sup> The Santa Clara Valley, north-west of Los Angeles also contains about 6,000 m of late Cenozoic strata that has been uplifted along the edges, deformed, and the top eroded off.<sup>14</sup> The South Caspian Basin, north-east of Iran, is about 450 km in diameter and has a total thickness of 26,000–28,000 m of sedimentary rocks.<sup>15</sup> Most of the sedimentary rocks in this basin are considered Cenozoic, with only the bottom layers possibly being Cretaceous.<sup>16</sup> The top 10,000 m alone are regarded as Pliocene and Quaternary, the very late Cenozoic.<sup>17,18</sup> All this huge amount of Cenozoic strata would have to be eroded from the surrounding mountains and transported in some cases hundreds of kilometres over low slopes. These magnitudes are powerful evidence of Flood activity and not of post-Flood catastrophism.

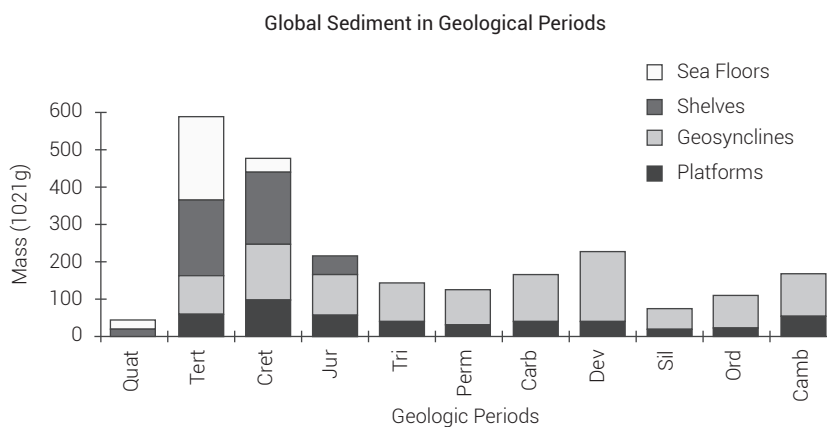
### Thin, widespread Cenozoic sedimentary layers

Many relatively thin, widespread layers are evident in the sedimentary rocks.<sup>19</sup> *Thin* and *widespread* of course are subjective, but the *magnitude* of some Cenozoic layers seems to defy any post-Flood mass wasting scenario. A layer a few hundred metres thick and covering 200,000 km<sup>2</sup> could be considered a thin, widespread layer. Some Cenozoic layers are of similar geographical extent and thickness to some Mesozoic formations, considered Flood sediments by Whitmore and myself.

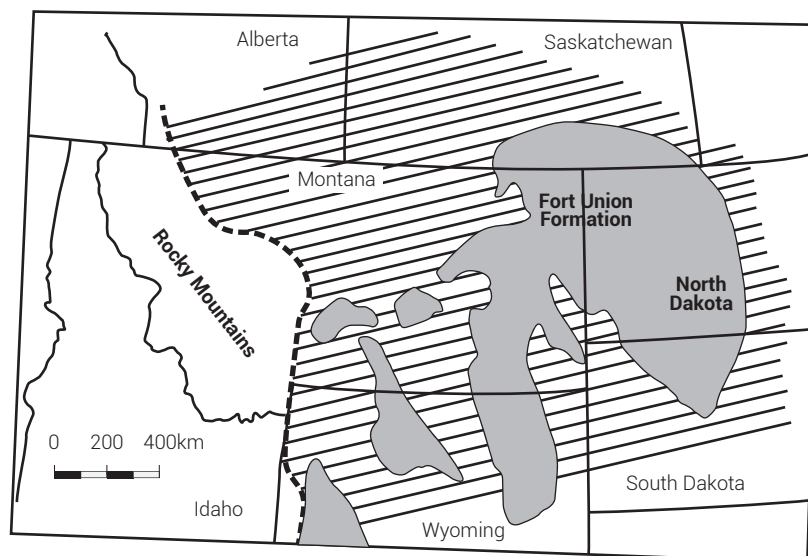
For example, the Fort Union Formation, assigned to the early Cenozoic, is composed of sandstone, shale, and coal, and outcrops over an area of about 150,000 km<sup>2</sup> (figure 2). If we include the area where it is supposed to have been eroded away, it is found to cover an additional 300,000 km<sup>2</sup>, making its total area 450,000 km<sup>2</sup>. The Fort Union Formation is about 300 m thick in eastern

**Table 1.** Summary of seven general features present in most Cenozoic sedimentary rocks best explained as a result of Flood processes. The strength measure against post-Flood formation and for Flood formation is based on the strength of current post-Flood explanations of these features.

Sedimentary Rock Evidences	Strength
1. Huge volume of Cenozoic sedimentary rocks	strong
2. Thin, widespread Cenozoic sedimentary layers	moderate
3. Consolidated Cenozoic sedimentary rocks	moderate
4. Deposition of widespread and/or thick Cenozoic 'evaporites'	strong
5. Cenozoic phosphorites	weak
6. Formation of Cenozoic carbonates	moderate
7. Tremendous Cenozoic continental margin sedimentary rocks	strong



**Figure 1.** Global distribution of Phanerozoic sediments by geological periods for four postulated paleoenvironments. The Cenozoic has been split into the Quaternary and Tertiary (from Holt<sup>11</sup>).



**Figure 2.** Extent of the Fort Union Formation (solid pattern) and the area from which uniformitarian scientists believe it was eroded (slanted pattern). The combined area is about 450,000 km<sup>2</sup> (drawn by Melanie Richard).

Montana and western North Dakota,<sup>20</sup> so it is relatively thin compared to its area. Whitmore and Garner have interpreted this formation as post-Flood, partly based on the presence of terrestrial fossils.<sup>2</sup> However, the Fort Union Formation covers a similar geographical area as some of the widespread, thin Mesozoic formations. The pre-erosion size of the Fort Union Formation was larger than the Shinarump Conglomerate (250,000 km<sup>2</sup>), similar in size to the Navajo Sandstone and its equivalents (400,000 km<sup>2</sup>), and half the area of the huge Morrison Formation (1 million km<sup>2</sup>). All of these latter three formations are assigned to the Mesozoic and all are considered Flood deposits.

Just because a formation contains terrestrial fossils does not mean that it was deposited in a terrestrial environment. This is an uniformitarian deduction, but in biblical earth history a terrestrial fauna can be catastrophically transported in the Flood and buried in a setting with few if any marine animals. And fossils that are normally considered marine are given a freshwater interpretation, such as ‘freshwater’ dinoflagellates and sponges found in the Miocene Clarkia beds of west-central Idaho.<sup>21</sup>

Moreover, there is additional evidence based on *isolated* erosional remnants above the Fort Union Formation that at least another 300 m of sedimentary rock, and probably much more (see section on lithification of sediments below), once laid on top of the Fort Union Formation and were subsequently eroded over a wide area. Sentinel Butte, just east of the Montana/North Dakota border, is a 300 m tall erosional remnant of horizontal strata (figure 3) that represents a much larger area of deposition over eastern Montana and western North Dakota.

Here is what must have happened if the Fort Union Formation is post-Flood. First, the deposit has to mass waste from some high area likely due to tectonic uplift. The Rocky Mountains, many hundreds of kilometres to the west and south-west, seem like the only major source of the huge volume of the Fort Union Formation before erosion (150,000 km<sup>3</sup>). The mountains east of the continental divide seem much too small to produce all this strata, not including the strata that once lay above the formation. Second, the mass wasting debris must spread out over an area of about 450,000 km<sup>2</sup> on the High Plains that have a low easterly slope. Mass wasting debris is generally considered of mixed particle sizes, while sandstone and shale are not normally considered mass wasting debris. Heavy precipitation could have caused fluvial sorting to produce the fine-grained sediments, in which case we should see abundant evidence of channels and other fluvial features. Mass wasting also produces thick deposits near the source, which thin distally. These features are rare at best in the Fort Union Formation. Third, dozens of nearly pure coal layers, some up to more than 60 m thick and laterally extensive, had to form during

mass wasting (Cenozoic coal will be discussed in a later part). Fourth, more strata was deposited on top of the Fort Union Formation—more than 300 m deep over at least eastern Montana and western North Dakota. Fifth, the strata must be lithified because near-vertically walled erosional remnants (figure 3) would not exist on top of the Fort Union Formation, if unconsolidated. Sixth, erosion by some mechanism (mass wasting?) takes away practically all the strata on top of the Fort Union Formation and the majority of the Fort Union Formation. Seventh, the erosional debris is not found downslope towards the Gulf of Mexico, but apparently has been completely swept off the continent and likely forms part of the strata down the topographic slope in southern Texas and the Gulf of Mexico. The Cenozoic strata younger than the Fort Union Formation downslope along the northern and central High Plains, the White River and Arikaree Groups, are predominantly volcanoclastic sediments reworked by water.<sup>22</sup> The surficial Miocene Ogallala Formation is predominantly sand and gravel eroded from the central and southern Rocky Mountains to the west. Without the sheer volume of water the Flood provided, such a scenario is quite implausible. Therefore, thin, widespread sedimentary layers in the Cenozoic present moderate difficulties for any attempt to explain them by post-Flood catastrophism.

### Consolidated Cenozoic sedimentary rocks

Another sedimentary criterion that can help determine the location of Flood/post-Flood boundary is the process of hardening or consolidation of sediments into sedimentary rocks.<sup>19</sup> Sediments are converted into sedimentary rock by a combination of compaction caused by burial (usually deep burial by hundreds of metres of sediment) and the



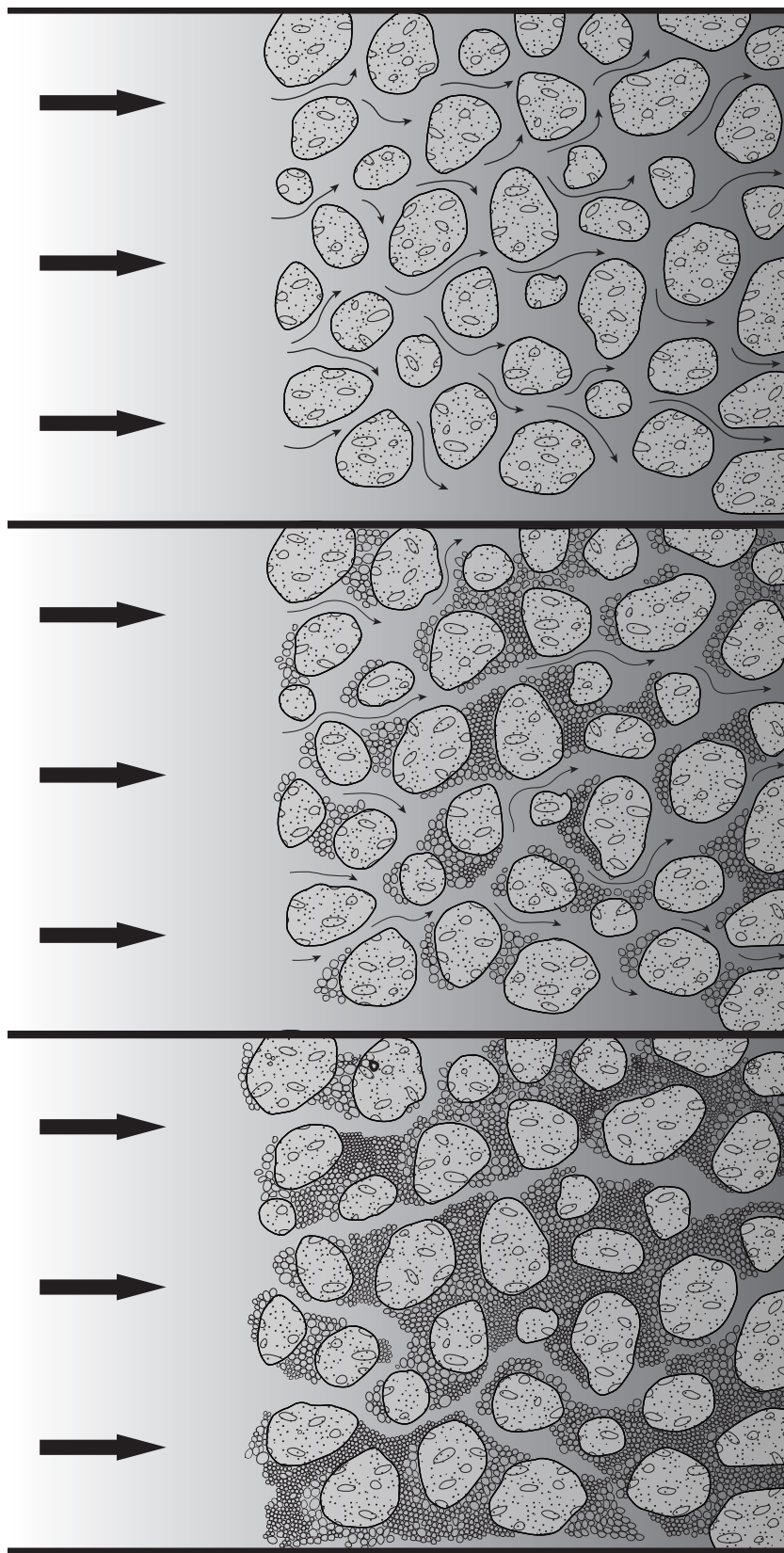
**Figure 3.** Sentinel Butte, western North Dakota, USA, is a flat-topped mesa about 300 m above the Fort Union Formation.

precipitation of cement within the pores around sediment grains.<sup>23</sup> However, cementation rarely occurs today because it requires special conditions and many variables.<sup>24,25,26</sup>

In order for cementing agents to permeate the sediments, water within the sediments containing dissolved chemicals must readily flow through the pore spaces, leaving a chemical residue behind. Cement attaches to the sedimentary grains and gradually fills up the pore spaces, decreasing the flow around the grains (figure 4). As the flow decreases, it is able to transport less cement into the sediment, so the process of cementation slows down with time. Sometime during this process, the sediment can be cemented enough to be considered a sedimentary rock. As such, it is possible for a sedimentary rock to vary in degree of cementation and in hardness due to the extent of cement growth, the type of mineral doing the cementation, the availability of cementing agents, and other variables. Time is only one of the many variables involved in lithification. The speed of cementation depends on the *right conditions*, and that is why even some pre-Cenozoic strata are poorly consolidated.

Calcite and silica, two very common minerals often found in cracks and veins in rock, are the main cementing agents. Iron oxides, other carbonate minerals, and clay minerals are minor agents. These dissolved minerals must flow through the pore spaces and precipitate in the voids between the grains. Sometimes even the grains themselves can dissolve in the lithification process and be re-deposited as cement or transported out of the particular sediment. For instance, after depositing a calcite cement, the pore water could change chemistry and dissolve the calcite or replace the calcite with another cementing mineral, such as dolomite.

The Genesis Flood rapidly deposited thick sediments, which were



**Figure 4.** Schematic of the cementing of sand into sandstone by water flowing through the pores and depositing cementing chemicals (drawn by Melanie Richard)



compacted rapidly because of the accumulation of hundreds to thousands of metres of sediments. The Flood would also have trapped abundant water within the sediment during deposition. Cementing chemicals could easily have been dissolved in hot water, both within the Flood water and in the water within the sediments. The rapid accumulation of sediments would force the chemically charged water to flow through the sediments under high overburden pressure.

In today's environment, both compaction and cementing agents are lacking,<sup>27</sup> creating a severe uniformitarian problem. Pettijohn states that in the lithification of a 100 m thick layer of sand, 25–30 m of cement must be deposited within the pore spaces (assuming little compaction).<sup>27</sup> But, the origin of this cement, and how and when the sediment is cemented, is unresolved:

“Cementation, moreover, is the last step in the formation of the sandstone, and our knowledge is incomplete and unsatisfactory unless the origin and manner of emplacement of the cement are fully understood. ... The problems of how and when sands become cemented and the source of the cementing material are still unresolved.”<sup>28</sup>

So, cementation by presently observed processes (uniformitarianism) is very difficult to explain. It has happened in the past under unexplained special conditions involving a lot of cementing agents; e.g. water with high concentrations of calcite or silica in some mines or hot springs.

Could deposition after post-Flood mass wasting in local to regional post-Flood catastrophes of Flood-laid sediments result in thick, lithified deposits? First, it is unlikely sediments at the end of the Flood would be thickly unconsolidated because *intense* Flood run-off, caused by the strong continental uplift and margin subsidence, would erode any unconsolidated sediment, leaving behind mostly lithified sediments. So, post-Flood mass wasting would be minor and could not erode and accumulate thousands of metres of sediments, either within the continental or along the continental margin. Second, the depositional products from mass wasting would have to be cemented. Chemicals need to be dissolved and flow through the pores of the mass wasted debris. Third, it is also impossible to know whether post-Flood catastrophes can create the special conditions required to dissolve cementing agents. It may be possible that the lower mass wasted sediments could be consolidated by compaction and cementation, but how would the top of the mass be also lithified?

Fully lithified sediments would likely have occurred during the Flood, while thin unconsolidated sediments would more likely occur after the Flood. Since Cenozoic sedimentary rocks are often lithified, such as the Fort Union Formation and Rocky Mountain basin strata, they present moderate difficulties for any attempt to explain them by post-Flood catastrophism.

### Deposition of widespread and/or thick Cenozoic ‘evaporites’

There are large and thick accumulations of ‘evaporites’ across the earth,<sup>29</sup> including salt (NaCl), anhydrite (CaSO<sub>4</sub>), and gypsum, which is the hydrated equivalent of anhydrite. These are found in layers and diapirs throughout the Phanerozoic sediments, including the Cenozoic. Unlike uniformitarian scientists, creationists do not believe these ‘evaporites’ represent evaporation from drying bodies of water but believe they were laid down rapidly by precipitation. Creationists, of course, need a detailed explanation for precipitates, and a few ideas have been posited, one being the igneous origin hypothesis.<sup>30</sup>

The largest ‘evaporite’ in the world is believed to be at the bottom of the Mediterranean Sea and has been locally uplifted a few thousand metres and exposed on land. It covers 2.5 million km<sup>2</sup> and averages 1 km deep.<sup>19</sup> The deepest section is about 3.5 km thick in the Herodotus Basin in the eastern Mediterranean Sea.<sup>31</sup> Uniformitarians call it the Messinian Salinity Crises and date it to the very late Miocene (late Cenozoic), about 5.5 million years ago. These evaporites are further overlain by about 1 km of Pliocene sediments or sedimentary rocks, indicating that significant geological activity occurred *after* the deposition of the salt and anhydrite.

This evaporite has inspired uniformitarian scientists to postulate that the Mediterranean Sea dried out dozens of times in the late Cenozoic. In a similar manner, the Red Sea also has thick late Miocene salt deposits that were probably deposited at the same time as in the Mediterranean Sea. Creationists, on the other hand, assume this ‘evaporite’ layer was deposited differently and in a shorter timeframe. However, the post-Flood argument falls short of explaining how such widespread deposits of salt and anhydrite were deposited, and it fails to explain how in turn they are overlain with a further 1 km of sediment. Such Cenozoic deposits present strong difficulties for any attempt to explain them as a result of post-Flood catastrophism.

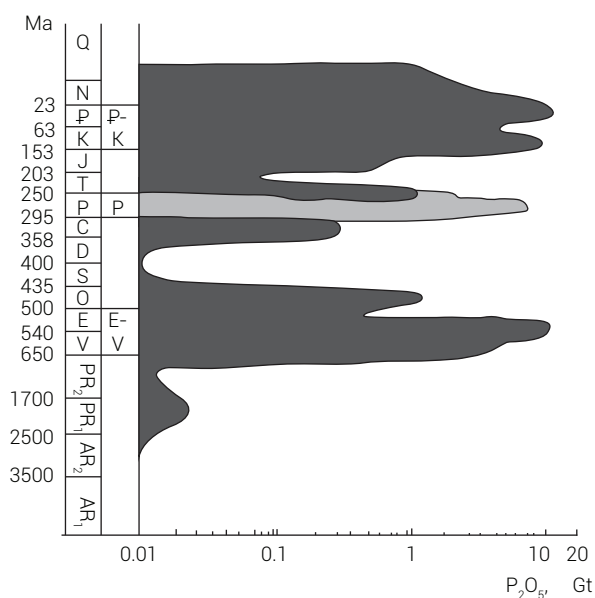
### Cenozoic phosphorites

Phosphorites are sedimentary rocks that contain a high concentration of phosphate, mostly as P<sub>2</sub>O<sub>5</sub>. The definition of a phosphorite is rather arbitrary, generally defined as over 19.5% phosphate, but high phosphate sedimentary rocks between 7.8% and 19.5% are of interest also. Many geologists would consider a rock as phosphatic if it contained 10 to 100 times more phosphate than normal. There are extensive layers of phosphorites, such as the Permian Phosphoria Formation and its equivalents in the northern Rocky Mountains of the United States that cover about 225,000 km<sup>2</sup>.<sup>32</sup> Uniformitarian scientists believe that

phosphorites originated as marine biochemical sedimentary rocks. They are believed to take thousands of years to form, and are rarely observed forming today.<sup>33</sup> Phosphorous (P) today is added to the sediments by coastal upwelling of P-rich bottom water and is extracted by marine organisms. When these organisms die, P is accumulated in the organic-rich bottom mud.<sup>34</sup> Bacteria help break down organic matter, forming phosphate in the sediments.<sup>33</sup>

Although phosphorites occur in the rock record as early as the early Proterozoic, they are especially concentrated in the Cretaceous and Cenozoic erathem, especially the Miocene series of the late Cenozoic (figure 5).<sup>35,36</sup> Föllmi and colleagues state:

“The Miocene was an epoch of preferential phosphogenesis and accumulation of phosphate-rich deposits, and Miocene phosphorites are widespread ...”<sup>37</sup>



**Figure 5.** Distribution of economic phosphorus resources in Earth history according to the evolutionary/uniformitarian timescale (modified by Melanie Richard from Kholodov and Butuzova<sup>36</sup>)

For instance, phosphate-rich sedimentary rocks of late Oligocene to late Miocene are found in Malta and south-east Sicily.<sup>38</sup> The early late Cenozoic (Miocene) Monterey Formation that outcrops over numerous areas of the coastal section between Los Angeles and San Francisco, California, has many high phosphate-rich layers.<sup>39</sup> Some of these are thin, persistent laminae.<sup>40</sup> Catastrophic deposition has been suggested:

“The concept of local catastrophic burial as a favourable prerequisite for the triggering of

phosphogenesis embodies a small-scale example of the importance of nonreversible, catastrophic events on geological and biological processes ...”<sup>41</sup>

Moreover, it is not enough to simply bury phosphate-rich organisms, as the phosphate needs to be *concentrated* in layers by transport within the interstitial water of the sediments. Evidence of subsurface movement of phosphate in pore water is shown by numerous examples of phosphatized fossils, coprolites (fossil dung), burrows, hardgrounds (hard cemented layers), etc.<sup>33,38</sup>

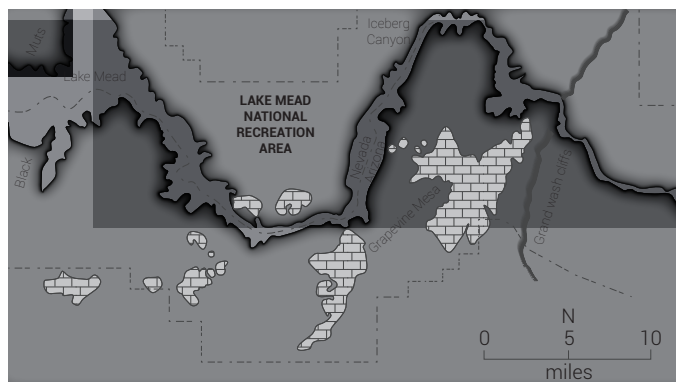
Could post-Flood catastrophes cause the quick formation of phosphorites? It seems rather doubtful that these catastrophes could bury enough organisms to result in much organic phosphate and be able to concentrate the phosphate into layers. Chances are such catastrophes would result in phosphate being randomly disseminated within the sediment, so that the concentration of P would be limited. Nonetheless, these difficulties for a post-Flood explanation are comparatively minor to other sedimentary features of the Cenozoic explored here, thus only provide modest evidence for Flood processes in the Cenozoic.

### Formation of Cenozoic carbonates

According to sedimentologist Francis Pettijohn, carbonates make up about 8% of all sedimentary rocks.<sup>42</sup> Carbonates are mostly calcite ( $\text{CaCO}_3$ ) and dolomite ( $\text{CaMgCO}_3$ ), which are minerals that precipitate out of water or are the remains of organisms with a carbonate shell extracted from seawater. They are abundant in the Paleozoic erathem and the Proterozoic (late Precambrian) and decrease upward in the geological column.<sup>43</sup>

Early Cenozoic carbonates can be widespread on the continents.<sup>44</sup> In North America, all of Florida is covered by early Cenozoic carbonate. In Central America, the Yucatan Peninsula is mostly early Cenozoic carbonate. In the Eastern Hemisphere, Saudi Arabia has large areas of early Cenozoic carbonates and larger areas are found in West Africa, East Africa, around the Mediterranean Sea, south-west Russia, and the Ukraine. Widespread Miocene carbonates of the late Cenozoic are found in the Caribbean Islands and the south-east United States in the Western Hemisphere.<sup>45</sup> Miocene carbonates are also found around the Mediterranean Sea, south-west Russia, and the Ukraine, but they are patchier than in the early Cenozoic. Some significant Miocene carbonates show up in Indonesia and southern Australia, as in the very flat Nullarbor Plain of South Australia covering 200,000 km<sup>2</sup>.<sup>46</sup>

An example of a late Cenozoic carbonate considered deposited in a terrestrial environment<sup>47</sup> is the top member of the Muddy Creek Formation of south-east Nevada and north-west Arizona, the Hualapai Limestone Member.<sup>48</sup>



**Figure 6.** Outcrops of the Hualapai Limestone Member of the Muddy Creek Formation in the Lake Mead area (drawn by Melanie Richard)

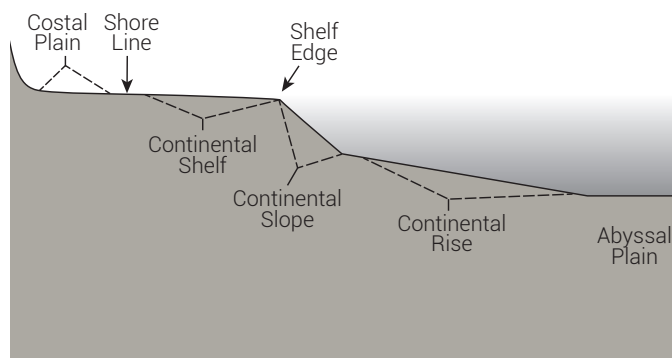
The Muddy Creek Formation is a basin-fill deposit that was deposited after uplift of the mountains.<sup>49</sup> The Hualapai Limestone Member is exposed in the Lake Mead area as limited erosional remnants that were originally deposited over a much larger area (figure 6). It not only forms thick masses but also is inter-bedded with other types of rocks, such as the conglomerates and sandstones of the Muddy Creek Formation.<sup>50</sup>

The Hualapai Limestone is over 300 m thick.<sup>51</sup> The volume of the current mass of limestone is over 100 km<sup>3</sup>.<sup>52</sup> However, its original volume would have been many times this volume since much of it has eroded. Its fine-grained nature suggests inorganic precipitation in water, although most uniformitarian scientists believe the carbonate originated from organisms because that is the type of carbonate predominantly forming today.<sup>53</sup> The limestone contains various types of fossils, including plant fossils of grasses, reeds, and rushes, and is one reason why some scientists have proposed a terrestrial origin.

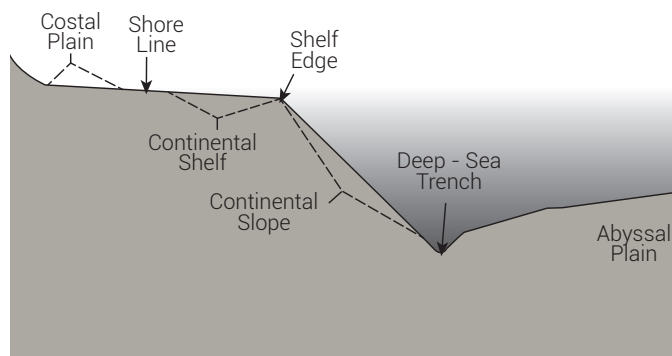
Significant inorganic carbonates are not forming in terrestrial environments today, but could they be deposited in postulated post-Flood catastrophic conditions? This is unlikely, as mass wasting would not result in thick, widespread, pure carbonates. But what of post-Flood lacustrine conditions? How can one explain where the carbonate came from? Given the nature of mass wasting processes one would think that any post-Flood limestone would be well mixed with other sediments, but these Cenozoic carbonates are relatively pure. Moreover, the top of the Hualapai Limestone has been eroded, so not only do advocates of post-Flood catastrophism need to deposit the limestone, but also to erode off the top. As such, large-scale Cenozoic carbonate deposits present moderate difficulties for any attempt to explain them by post-Flood catastrophism.

### Extensive Cenozoic continental margin sedimentary rocks

The continental margin includes the shallow, seaward-dipping continental shelf, the continental slope, and in offshore areas without trenches the continental rise (figure 7). The continental margin represents a thick accumulation of sedimentary rocks that form a continuous ring around the continents and large islands of the earth. The profile is very similar across the earth with the depth close to 130 m at the 'slope break', except the Antarctic margin that is isostatically depressed from the ice sheet. The continental shelf can be very wide; e.g. up to 1,500 km wide north of Siberia. Below the continental margin sedimentary rocks there are many buried rifts or basins that were caused by extension and subsidence. The Cenozoic and late Mesozoic sedimentary rocks reach over 20 km deep in places.<sup>54</sup> Based on seismic profiles, it appears that many of the sediments were deposited by transport *off* the continents, not by the longshore currents that commonly run parallel to most shorelines today. Monteverde *et al.* state:



**Figure 7a.** Schematic of an Atlantic-type continental margin (drawn by Melanie Richard)



**Figure 7b.** Schematic of a Pacific-type continental margin (drawn by Melanie Richard)



“Seismic profiles show that the New Jersey continental shelf contains a thick record of prograding clinoform wedges. ... Similar prograding clinoform wedges are observed in Neogene [late Cenozoic] sediments of passive and active margins throughout the world ...”<sup>55</sup>

This prograding wedge of sedimentation implies currents that rushed directly off the continents and can readily be explained by sheet flow, resulting in sheet deposition in waning currents, during Flood run-off from the continents.

Continental margins contain a large proportion of Cenozoic sedimentary rocks. The rest are from the upper half of the Mesozoic. For instance, off the central East Coast of the United States it has been estimated that out of a total volume of 1.34 million km<sup>3</sup> of sedimentary rocks about 30% are of Cenozoic age.<sup>56</sup> The very thick continental margin in the northern Gulf of Mexico is filled with about 12 km of Cenozoic sedimentary rocks.<sup>57</sup> The central Argentine continental margin, 150–500 km wide, contains one of the thickest accumulations of sedimentary rocks in the world.<sup>58,59</sup> Based on the inferred age of the sedimentary rocks from seismic profiles, about 50–75% of these sediments are dated as Cenozoic. The Mediterranean Sea off Israel has a maximum of about 5 km of Cenozoic sedimentary rocks.<sup>60</sup> Two basins on the South China Sea continental margin contain Cenozoic sedimentary rocks greater than 10 km thick.<sup>61</sup> It appears that about 40% of the sedimentary rocks on the continental margin off the west coast of South Africa are Cenozoic deposits.<sup>62</sup>

Therefore, Cenozoic strata along the continental margin represents at least a few thousand metres of deposition. If these strata were deposited after the Flood, mass wasting would have to remove thousands of metres of rock from the uplifting continents. The sediments must then be transported to the continental margin. Along some continental margins, such as north of Siberia, mountains where mass wasting could occur are generally far from the coast. The deposition would have to form a *continuous* sheet around all the continents and large islands with a near constant depth for the slope break. How can the universal characteristics of the continental margin possibly be explained after the Flood with local or regional mass wasting events and giant floods? In light of the stiff difficulties facing any potential post-Flood explanation of the sheer amount of Cenozoic sedimentary rocks on the continental margin, this counts as strong evidence for these Cenozoic rocks resulting from Flood processes.

## Conclusion

Whitmore and other creation scientists have claimed that the main evidence for attributing most of the Cenozoic

to Flood processes relies on geomorphology. However, there are numerous non-geomorphological features of the Cenozoic rocks that suggest most were formed by Flood processes. Sedimentary features of the Cenozoic rock record are better explained with reference to Flood processes than post-Flood catastrophism including: the sometimes great thicknesses; sometimes widespread, thin deposition; the consolidation of sediments; widespread or thick ‘evaporites’; phosphorites; carbonates; and thick continental margin strata. All these features support the contention that the Flood/post-Flood boundary is predominantly in the late Cenozoic, and likely in the very late Cenozoic in many areas.

## References

1. Whitmore, J.H., The potential for and implications of widespread post-Flood erosion and mass wasting processes; in: Horstemeyer, M. (Ed.), *Proceedings of the Seventh International Conference on Creationism*, Creation Science Fellowship, Pittsburgh, PA, 2013.
2. Whitmore, J.H. and Garner, P., Using suites of criteria to recognize pre-Flood, Flood, and post-Flood strata in the rock record with application to Wyoming (USA); in: Snelling, A.A. (Ed.), *Proceedings of the Sixth International Conference on Creationism*, Creation Science Fellowship, Pittsburgh, PA, pp. 425–448, 2008.
3. Whitmore, J.H. and Wise, K.P., Rapid and early post-Flood mammalian diversification evidences in the Green River Formation; in: Snelling, A.A. (Ed.), *Proceedings of the Sixth International Conference on Creationism*, Creation Science Fellowship, Pittsburgh, PA, pp. 449–457, 2008.
4. Oard, M.J. and Whitmore, J.H., The Green River Formation of the west-central United States: Flood or post-Flood? *J. Creation* **20**(1):46–85, 2006.
5. Whitmore, J.H., The Green River Formation: a large post-Flood lake system, *J. Creation* **20**(1):55–63, 2006.
6. Oard, M.J. and Klevberg, P., Green River Formation very likely did not form in a postdiluvial lake, *Answers Research Journal* 1:99–107, 2008.
7. Neuendorf, K.K., Mehl, Jr., J.P. and Jackson, J.A., *Glossary of Geology*, 5<sup>th</sup> edition, American Geological Institute, Alexandria, VA, p. 397, 2005.
8. Oard, M.J., (ebook) *The Flood/Post-Flood Boundary Is in the Late Cenozoic with Little Post-Flood Catastrophism* 2014, michael.oards.net/PostFloodBoundary.htm.
9. Wise, K.P., Austin, S.A., Baumgardner, J.R., Humphreys, D.R., Snelling, A.A. and Vardiman, L., Catastrophic plate tectonics: a global Flood model of earth history; in: Walsh R.E. (Ed.), *Proceedings of the Third International Conference on Creationism*, technical symposium sessions, Creation Science Fellowship, Pittsburgh, PA, pp. 609–621, 1994.
10. Oard, M.J., Is the K/T the post-Flood boundary?—part 1: introduction and the scale of sedimentary rocks, *J. Creation* **24**(2):95–104, 2010.
11. Holt, R.D., Evidence for a late Cainozoic Flood/post-Flood boundary, *J. Creation* **10**(1):128–167, 1996.
12. Elders, W.A., Rex, R.W., Meidav, T., Robinson, P.T. and Biehler, S., Crustal spreading in Southern California, *Science* **178**:15–24, 1972.
13. Ingersoll, R.V. and Rumelhart, P.E., Three-stage evolution of the Los Angeles basin, southern California, *Geology* **27**(7):593–596, 1999.
14. Sharp, R.P., *Southern California*, Kendal/Hunt Publishing Company, Dubuque, IA, p. 13, 1975.
15. Knapp, C.C., Knapp, J.H. and Connor, J.A., Crustal-scale structure of the South Caspian Basin revealed by deep seismic reflection profiling, *Marine and Petroleum Geology* **21**:1073–1081, 2004.
16. Artyushkov, E.V., Formation of the superdeep South Caspian basin: subsidence driven by phase change in continental crust, *Russian Geology and Geophysics* **48**:1002–1014, 2007.
17. Pawlak, A., Eaton, D.W., Bastow, I.D., Kendall, J.-M., Helffrich, G., Wookey, J. and Snyder, D., Crustal structure beneath Hudson Bay from ambient-noise tomography: implications for basin formation, *Geophysical Journal International* **184**:65–82, 2011.
18. Richardson, S.E.J., Davies, R.J., Allen, M.B. and Grand, S.F., Structure and evolution of mass transport deposits in the South Caspian Basin, Azerbaijan, *Basin Research* **23**:702–719, 2011.

19. Oard, M.J., Defining the Flood/post-Flood boundary in sedimentary rocks, *J. Creation* **21**(1):98–110, 2007.
20. Belt, E.S., Hartman, J.H., Diemer, J.A., Kroeger, T.J., Tibert, N.E. and Curran, H.A., Unconformities and age relationships, Tongue River and older members of the Fort Union Formation (Paleocene), western Williston Basin, U.S.A., *Rocky Mountain Geology* **39**(2):113–140, 2004.
21. Oard, M.J., A uniformitarian paleoenvironmental dilemma at Clarkia, Idaho, USA, *J. Creation* **16**(1):3–4, 2002.
22. Terry, D.O., LaGarry, H.E. and Hunt, Jr., R.M. (Eds.), Depositional Environments, Lithostratigraphy, and Biostratigraphy of the White River and Arikaree Groups (late Eocene to early Miocene, North America), *GSA Special Paper 325*, Geological Society of America, Boulder, CO, 1998.
23. Plummer, C.C. and McGary, D., *Physical Geology*, 7<sup>th</sup> edn, Wm. C. Brown Publishers, Dubuque, IA, p. 117, 1996.
24. McBride, E.F., Quartz cement in sandstones: a review, *Earth-Science Reviews* **26**:69–112, 1989.
25. Haddad, S.C., Worden, R.H., Prior, D.J. and Smalley, P.C., Quartz cement in the Fontainebleau Sandstone, Paris Basin, France: crystallography and implications for mechanisms of cement growth, *Journal of Sedimentary Research* **76**:244–256, 2006.
26. Molenaar, N., Cyziene, J. and Sliupa, S., Quartz cementation mechanism and porosity variation in Baltic Cambrian sandstones, *Sedimentary Geology* **195**:135–159, 2007.
27. Pettijohn, F.J., *Sedimentary Rocks*, 3<sup>rd</sup> edn, Harper and Row, New York, pp. 239–245, 1975.
28. Pettijohn, ref. 27, pp. 239, 242.
29. Warren, J.K., Evaporites through time: tectonic, climatic and eustatic controls in marine and nonmarine deposits, *Earth-Science Reviews* **98**:217–268, 2010.
30. Heerema, S., A magmatic model for the origin of large salt formations, *J. Creation* **23**(3):116–118, 2009; creation.com/magmatic-origin-salt-deposits
31. Rouchy, J.M. and Caruso, A., The Messinian salinity crisis in the Mediterranean basin: a reassessment of the data and an integrated scenario, *Sedimentary Geology* **188–189**:35–67, 2006.
32. Piper, D.Z., Marine chemistry of the Permian Phosphoria Formation and basin, south-east Idaho, *Economic Geology* **96**:599–620, 2001.
33. Föllmi, K.B., The phosphorus cycle, phosphogenesis and marine phosphate-rich deposits, *Earth-Science Reviews* **40**:55–124, 1996.
34. Nelson, G.J., Pufahl, P.K. and Hiatt, E.E., Paleooceanographic constraints on Precambrian phosphorite accumulations, Baraga Group, Michigan, USA, *Sedimentary Geology* **226**:9–21, 2010.
35. Nelson *et al.*, ref. 34, p. 17.
36. Kholodov, V.N. and Butuzova, G. Yu., Problems of iron and phosphorus geochemistry in the Precambrian, *Lithology and Mineral Resources* **36**(4):293, 2001.
37. Föllmi, K.B., Hofmann, H., Chiaradia, M., de Kaenel, E., Frijia, G. and Parente, M., Miocene phosphate-rich sediments in Salento (southern Italy), *Sedimentary Geology* **327**:55, 2015.
38. Föllmi, K.B., Gertsch, B., Renevey, J.-P., De Kaenel, E. and Stille, P., Stratigraphy and sedimentology of phosphate-rich sediments in Malta and south-eastern Sicily (latest Oligocene to early late Miocene), *Sedimentology* **55**:1,029–1,051, 2008.
39. Berndmeyer, C., Birgel, D., Brunner, B., Wehrmann, L.M., Jöns, N., Bach, W., Arning, E.T., Föllmi, K.B. and Peckmann, J., The influence of bacterial activity on phosphorite formation in the Miocene Monterey Formation, California, *Palaeogeography, Palaeoclimatology, Palaeoecology* **317–318**:171–181, 2012.
40. Föllmi, K.B. and Garrison, R.E., Phosphatic sediments, ordinary or extraordinary deposits? The example of the Miocene Monterey Formation (California); in: Miller, D.W., McKenzie, J.A., and Weissert H. (Eds.), *Controversies in Modern Geology: Evolution of Geological Theories in Sedimentology, Earth History and Tectonics*, Academic Press, New York, pp. 55–84, 1991.
41. Föllmi and Garrison, ref. 40, p. 55.
42. Pettijohn, ref. 27, p. 22.
43. Pettijohn, ref. 27, p. 317.
44. Ronov, A.B., Khain, V.Ye. and Balukhovskiy, A.N., Paleogene lithologic associations of the continents, *International Geology Review* **21**(4):415–446, 1979.
45. Khain, V.Ye., Ronov, A.B. and Balukhovskiy, A.N., Neogene lithologic associations of the continents, *International Geology Review* **23**(4):426–454, 1981.
46. Twidale, C.R. and Campbell, E.M., *Australian Landforms: Understanding a Low, Flat, Arid and Old Landscape*, Rosenberg Publishing Pty Ltd, New South Wales, Australia, p. 153, 2005.
47. Hunt, C.B., Cenozoic Geology of the Colorado Plateau, *U.S. Geological Survey Professional Paper 279*, U.S. Government Printing Office, Washington, D.C., 1956.
48. Blair, W.N. and Armstrong, A.K., Hualapai Limestone Member of the Muddy Creek Formation: the Youngest Deposit Predating the Grand Canyon, South-eastern Nevada and North-western Arizona, *U.S. Geological Survey Professional Paper 1111*, U.S. Government Printing Office, Washington, D.C., 1979.
49. Dicke, S.M., Stratigraphy and sedimentology of the Muddy Creek Formation, south-eastern Nevada, M.S. thesis, University of Kansas, Lawrence, KS, 1985.
50. Young, R.A., Pre-COLORADO River drainage in western Grand Canyon: potential influence on Miocene stratigraphy in Grand Wash Trough; in: Reheis, M.C., Hershler, R. and Miller, D.M. (Eds.), *Late Cenozoic Drainage History of the South-west Great Basin and Lower Colorado River Region: Geologic and Biotic Perspectives*, *GSA Special Paper 439*, Geological Society of America, Boulder, CO, pp. 319–333, 2008.
51. Hunt, ref. 47, pp. 33, 35.
52. Blair and Armstrong, ref. 48, p. 12.
53. Blair and Armstrong, ref. 48, p. 9.
54. Deptuck, M.E., MacRae, R.A., Shimeld, J.W., Williams, G.L. and Fensome, R.A., Revised Upper Cretaceous and lower Paleogene lithostratigraphy and depositional history of the Jeanne d'Arc Basin, offshore Newfoundland, Canada, *AAPG Bulletin* **87**(9):1,459–1,483, 2003.
55. Monteverde, D.H., Miller, K.G. and Mountain, G.S., Correlation of offshore seismic profiles with onshore New Jersey Miocene sediments, *Sedimentary Geology* **134**:111–127, 2000.
56. Poag, C.W., U.S. Middle Atlantic Continental Rise: Provenance, Dispersal, and Deposition of Jurassic to Quaternary Sediments; in: Poag, C.W. and de Graciansky P.C. (Eds.), *Geological Evolution of Atlantic Continental Rises*, Van Nostrand Reinhold, New York, pp. 100–156, 1992.
57. Bally, A.W., Phanerozoic basins of North America; in: Bally, A.W. and Palmer A.R. (Eds.), *The Geology of North America—An Overview, The Geology of North America, volume A*, Geological Society of America, Boulder, CO, pp. 397–446, 1989.
58. Hinz, K., Neben, S., Schreckenberger, B., Roeser, H.A., Block, M., Goncalves de Souza, K. and Meyer, H., The Argentine continental margin north of 48°S: sedimentary successions, volcanic activity during breakup, *Marine and Petroleum Geology* **16**:1–25, 1999.
59. Gruetznier, J., Uenzelmann-Neben, G. and Franke, D., Variations in sediment transport at the central Argentine continental margin during the Cenozoic, *Geochemistry, Geophysics, Geosystems* **13**(10):1–15, 2012.
60. Steinberg, J., Gvirtzman, Z., Folkman, Y. and Garfunkel, Z., Origin and nature of the rapid late Tertiary filling of the Levant Basin, *Geology* **39**:355–358, 2011.
61. Xie, X., Dietmar Müller, R., Ren, J., Jiang, T. and Zhang, C., Stratigraphic architecture and evolution of the continental slope system in offshore Hainan, northern South China Sea, *Marine Geology* **247**:129–144, 2008.
62. Wigley, R.A. and Compton, J.S., Late Cenozoic evolution of the outer continental shelf at the head of the Cap Canyon, South Africa, *Marine Geology* **226**:1–23, 2006.

**Michael J. Oard** has an M.S. in atmospheric science from the University of Washington and is now retired after working as a meteorologist with the US National Weather Service in Montana for 30 years. He is the author of *Frozen in Time, Ancient Ice Ages or Gigantic Submarine Landslides?, Flood by Design, Dinosaur Challenges and Mysteries, and Exploring Geology with Mr. Hibb.* He serves on the board of the *Creation Research Society*.

# Origins of pathogenic microbes: part 1—bacteria

Warren A. Shipton

The emergence of pathogenic bacteria interests creationists because it impacts on concepts of God's character. The ecosystem operated in a stable fashion at creation and the basic microbe types participated in maintaining a dynamic homeostatic state. Sin brought a change to features of DNA repair and gene regulation in living systems, and stress was introduced into the equation. This resulted in mutations and other errors giving rise to cellular malfunctions. Mechanisms permitting re-assortment and exchange of genetic material within precise limits were disrupted. Most of these mechanisms are well known, but additional ones have been described recently and more may be discovered. Reasonable hypotheses are generated to account for the emergence of the main groups of pathogenic bacteria by unguided events involving genetic material. These involve events in the microbe, in the host, and changes in the environment. Subsequent to the Fall, changes to living organisms and the ecosystem usually are not considered dependent on the direct activity of God. However, other external agencies could have been involved.

The biblical account of origins indicates that creation was very good. The origin of pathogens causing suffering, disease, and death is a challenging question. A number of possibilities have been suggested as follows: 1) micro-organisms (including viruses) were not disease-causing initially. They devolved after creation as a result of mutation and gene shuffling among themselves. As a consequence a small number of pathogenic variants arose,<sup>1</sup> 2) God created pathogens in the lower orders of life to ensure population control, but this did not extend to microbes inhabiting humans. Rather, mutations gave rise to pathogens among populations of usually beneficial microbes inhabiting the human body and similar mutations in animal pathogens enabled them to jump the species barrier and infect humans,<sup>2</sup> 3) the genomes of all creatures were designed so that they could adapt rapidly to the environment. These variant-producing DNA segments have become compromised, giving rise to RNA viruses and perhaps retroviruses, ostensibly on account of the removal of the 'regenerating healing power' of God,<sup>3</sup> 4) diversity can be accounted for by postulating that transposable elements were originally designed to produce positive altruistic outcomes, but subsequently caused near neutral, or even deleterious, mutations,<sup>4</sup> and 5) microbes were not initially disease-causing in creatures with pain sensations but as a consequence of various changes they appeared, perhaps assisted by exterior agencies.

Change after the Fall conceivably involved shifts in ecosystem balance so that the nature and behaviour of organisms was altered. In an extension of the suggestion about agencies, some have postulated that an evil agent(s) altered or added novel genetic information to the genome

of existing organisms or an entirely new line of microbes was allowed to emerge (God's Curse).<sup>5</sup>

To answer these proposals, several assumptions are made. Undoubtedly, some of these will be challenged as knowledge increases. The most significant is that the existence of beneficial phenomena in the natural world that are widely expressed will be taken to indicate their essential continuity from the beginning (parsimonious approach), except where biblical information dictates otherwise.

## Events promoting the rise of pathogens?

The vast majority of microbes do not inflict damage on their hosts. They are non-pathogenic. The majority of microbes inhabiting humans are classically harmless commensals (one organism benefits, the other is not harmed or benefited).<sup>6</sup> Microbes are present in large numbers in and on the human body and ensure our survival. They aid digestion and provide nutrients necessary for our well-being. In herbivores, they are absolutely vital for cellulose digestion and the provision of some of the protein needs. Microbes that cause damage are called pathogens. However, disease does not depend alone on the microbe acquiring special abilities such as toxin genes. Three factors contribute to the expression of disease—microbe, host, and environment.<sup>7</sup>

Microbes that exhibit polysaccharide capsules (figure 1), toxin- and melanin- forming features, tissue-invading (enzyme) capabilities, and other characteristics frequently are pathogenic. These may have arisen as a consequence of a variety of events. First, elements of the gene regulatory network, particularly the non-coding region of the chromosome, may have been altered. As a consequence,



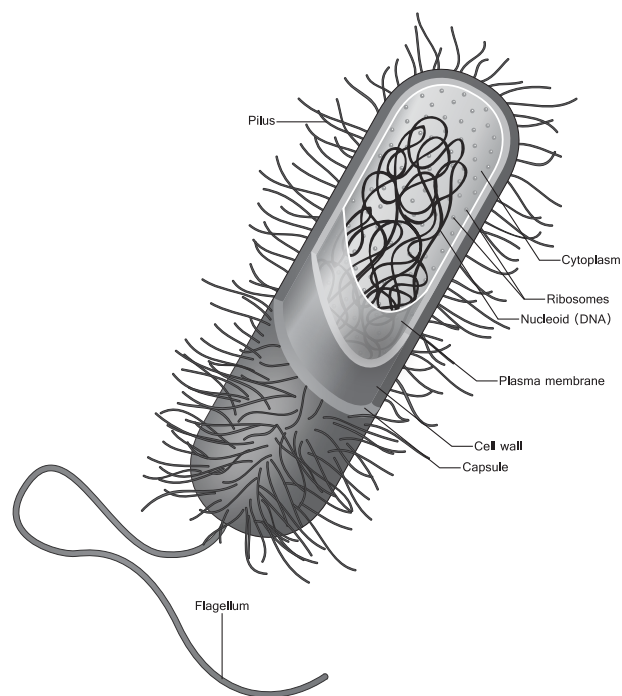
feedback processes, dominant metabolic pathways, and other aspects of cellular function were altered in the host or microbe.<sup>8</sup> Second, microbes in mutualistic (organism and host benefit from association) and endosymbiotic associations (living inside another organism) may have been modified through degenerative and other changes. Third, saprophytic equivalents (free-living on dead material) to the present-day pathogens may have been created and have subsequently acquired pathogenic abilities. Fourth, genes may have been lost that enabled the expression of pathogenic ability. Fifth, changes may have occurred in the host, allowing opportunistic organisms to become pathogenic. Sixth, organisms may have adapted under environmental stress or changes in nutrition, facilitating the appearance of pathogens.<sup>9</sup> Seventh, intelligent agents may have manipulated the genetic material.<sup>10</sup> Finally, there may have been a combination of the above events.

In environments containing a diversity of organic materials rich in DNA, and where microbial growth and decay activities are intense, it is more likely that organisms exchange genetic information.<sup>11</sup> Mechanisms known today, including recombination during sexual reproduction, transduction, transformation, and non-random transposition are considered to have been present from creation. Mutations were probably also known then. There are different categories of mutations.<sup>12</sup> Those commonly encountered today arise frequently through exposure of the organism to stress (chemical, nutritional, and physical factors). DNA is damaged and the repair mechanisms are unable to rectify the faults, meaning that imprecision in nucleic acid copying occurs. The entire operational strategy set in motion at creation changed after sin's entrance so that future outcomes were foreseen, but are not attributable to the Planner.

### Genesis and expression of pathogenic capabilities

Virulence (relative ability to cause disease) is not strictly an intrinsic microbial characteristic but includes both microbial and host factors. This conclusion is reached on account of commensals and opportunists being able to cause disease in the immunocompromised. In retrospect, the factors classically related to virulence, such as toxicity, aggressiveness, replication and transmission advantages, adherence and attachment, and induction of deleterious immunologic reactions,<sup>13</sup> still have relevance.

Changes in colonising status, such as the ability to cause disease, ultimately indicate changes in DNA, gene regulatory network elements and other features. DNA repair mechanisms are variously subject to imperfections so that variant DNA appears. As a result some viable mutants are generated. For example, bacteria may experience mutations on account of damage to their mismatch repair system.



**Figure 1.** A schematic diagram of a bacterium showing various structures including a polysaccharide capsule.

These mismatch defects may subsequently be removed, but the mutations generated during the period of high mutation are retained.<sup>14</sup> Changes in proteins coded by the genome are expressed through the regulatory elements that involve feedback processes, dominant metabolic pathways, and other features. If the right combination of virulence factors is present in an organism (many of which may be present already in non-pathogenic organisms), then cross talk among virulence factors may result in regulatory changes leading to the actual expression of virulence.<sup>15</sup>

Changes may also occur in the non-coding region of the chromosome near the promoter (regulator changes). This would cause gene expression levels to be altered in the host or microbe. Sin's entrance may have altered the repair mechanisms' efficiency due to the stresses introduced and may also have involved changes in the regulatory elements.

An example involves the well-known bacterium *Escherichia coli*. Its effectiveness as a gut pathogen is influenced by the DNA modifications (base methylation) which affect the production of an appropriate attachment device (pilus—figure 1). This plays a role in disease development. Methylation levels (represents an epigenetic control mechanism) are governed by the growth conditions of the organism. In other bacteria, virulence is partly lost when methylation fails to occur or is overproduced.<sup>16</sup> Theoretically, an organism could be benign, but after the removal of the silencing effects on a gene (influenced by methylation state), it could become pathogenic.<sup>17</sup>

## Microbe changes

Microbes as a group can function in almost all environments and carry out a wide range of activities. Theoretically some microbes could adapt to the pathogenic mode of existence. Selected examples follow.

*Mutualistic and endosymbiotic organisms.* Altering mutualistic organisms to take on parasitic capabilities is one possibility, as they already possess host entry mechanisms and strategies to acquire nourishment. The rhizobia bacteria are mutualistic with leguminous plants. Special genes (*bac*) enable them to form intracellular structures, permitting the fixation of atmospheric nitrogen. These genes have a high degree of similarity with those found in *Brucella*, a well-known intracellular animal pathogen, which allows it to survive in the phagocytic cells of the animal host. In addition, *Brucella*'s regulatory system for virulence has remarkable similarities to certain genes found in the harmless mutualist (*Sinorhizobium meliloti*).<sup>18</sup> The plant bacterium *Agrobacterium*, commonly considered a pathogen, could have acquired many of its capabilities from rhizobia.<sup>19</sup> How the acquisition occurred is a separate issue.

The bacterium *Wolbachia* has achieved prominence on account of its apparent ability to transfer information to insect and nematode hosts. For example, the fruit fly (*Drosophila ananassae*) has the entire genome of the endosymbiotic bacterium inserted into one of its chromosomes.<sup>20</sup> These symbionts influence reproductive success and strategy in insects.

Research on the *Wolbachia* genome has been taken by some to suggest that endosymbionts have acquired this ability through the loss of critical genes needed for growth independent of a host.<sup>21</sup> However, introducing *Wolbachia* into the mosquito is connected to the development of resistance of this insect to transmitting a devastating form of malaria.<sup>22</sup> This may indicate that endosymbionts had some protective role from creation and that their present genome imperfectly represents the original.

## Saprophytes

Many saprophytic microbes are beneficial to other organisms.<sup>23</sup> Normally harmless inhabitants of the soil can become pathogenic under certain favourable environmental conditions. Soil saprophytes also often possess capsules from which the capsule-forming ability of successful pathogens may have been derived.<sup>24</sup> These opportunists also become pathogenic when the host defences are breached or compromised<sup>25</sup> or when the organism is introduced into the body following prosthesis implantation and the insertion of catheters.<sup>26</sup>

*Bacillus* is an example of a saprophyte that has pathogenic representatives. Some members are pathogenic, such as *B. anthracis*, the causal agent of classical anthrax. It is

pathogenic due to its capsule-forming and toxin-generating capacities. Capsule formation is conferred by transfer of extrachromosomal DNA material in plasmids and subsequent modification. Toxin genes are also plasmid borne. An acquisition route for the saprophyte has been indicated by studying a close relative of *Bacillus cereus* capable of causing anthrax in chimpanzees.

*B. cereus* appears to be a normal inhabitant of the intestines of soil-dwelling insects and earthworms and may be useful partners with other insects.<sup>27</sup> One possibility is that the anthrax-forming *B. cereus* originally had a well-established role in the soil. Transformation (uptake of naked nucleic acid) or transduction (transfer of genetic information by phage), involving acquisition of plasmids (containing genes that produce toxin) from *B. anthracis*, apparently gave *B. cereus* the ability to induce anthrax-like symptoms. Acquisition can occur ostensibly in soil or during co-infection of the host.<sup>28</sup>

*Mutations.* Virulence may arise through mutations, which are expressed in a number of ways. Gene loss may lead to the emergence of pathogenic ability. The *cadaverine* gene (lysine decarboxylase activity) is able to prevent toxin production. The majority of *Escherichia coli* strains possess this gene, which appears to be connected with their commensal status in the human gut. When *cadaverine* gene activity is lost in certain strains of *Escherichia coli* (EIEC) they develop pathogenic ability. The loss of activity is associated with large deletions in the chromosome region around the *cadaverine* locus. This means that toxin production henceforth can be expressed.<sup>29</sup> Again, in *Listeria monocytogenes*, mutation of a critical gene associated with a regulatory protein may lead to changes whereby the normally saprophytic organism can become constitutively pathogenic.<sup>30</sup>

## Host changes

The best-known example of host changes leading to disease is the process that causes immunocompromisation. These hosts may be predisposed to attack from organisms not normally considered pathogens. Sometimes around half of such individuals experience bacterial infections. For example, the usually saprophytic bacterium *Nocardia* can be a significant cause of illness.<sup>31</sup>

Environmental influences facilitate emergence and expression of change

Changes in the environment may be responsible for the emergence and expression of virulence traits. Several examples will be given in each category.

*Emergence.* Adaptive mutations may occur in response to environmental stresses. Opportunistic pathogens in the *Burkholderia cepacia* complex affect cystic fibrosis and

immunocompromised patients. They may adapt through exposure to antibiotics and other stress conditions. These variants are more suited to colonise the lungs of fibrosis sufferers and contribute to disease progression.<sup>32</sup>

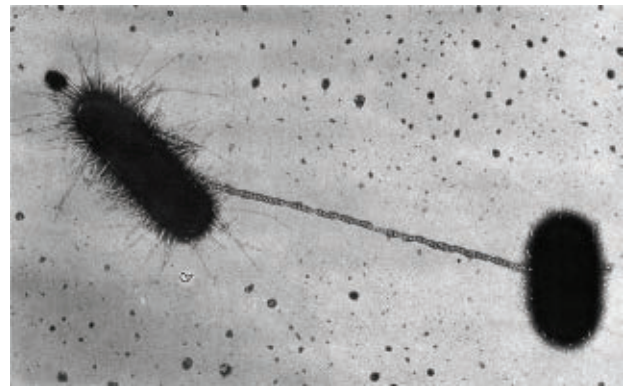
During stress, mechanisms normally controlling transfer of information horizontally between organisms may be relaxed due to the inactivation of the methyl-directed mismatch repair system. The system can be damaged through exposure to starvation conditions, for instance. Change in this repair system increases the mutation rate substantially, causing hypermutation, and as a result greatly increases the recombination success between *Escherichia* and *Salmonella*. This may represent one mechanism responsible for the appearance of virulence genes in the food poisoning bacterium *Escherichia coli* (O157:H7) from another strain of the same organism.<sup>33</sup> However, a number of other possibilities have been suggested in the genesis of the strain.<sup>34</sup>

**Expression.** Some microbes are not pathogens when biological balance is maintained in a natural environment. But saprophytic bacteria responding to change may damage potential hosts. For example, *Acinetobacter baumannii* is significant in wound situations and airway infections in alcoholics. In hospital situations where ethanol (alcohol) is used as a disinfectant, it can function as a nutrient that increases the virulence of the organism by the differential expression of certain genes. The nutrient may also influence the expression of tissue receptors, which would then initiate intracellular signalling, leading to differential gene expression and heightened tissue responses that allow increases in tissue damage by the microorganism.<sup>35</sup> The bacterium *Agrobacterium tumefaciens* (commonly saprophytic in soils) also displays a similar pattern of virulence induction. The organism becomes pathogenic to plants following exposure to phenolic substances and/or saccharides released. Sensing these products occurs at the membrane level, by sensory proteins, and ultimately to the activation of promoters. The inducing sugars may be released by wounded tissues.<sup>36</sup>

### Mechanisms for transfer of genetic information

There are well-known methods for horizontal transfer of information among bacteria, including transformation (uptake of external DNA through the cell membrane), transduction (transfer by bacterial viruses or phages), and sexual reproduction (referred to as conjugation between closely related types—figure 2). Less well-known is transfer through membrane vesicles and intercellular nanotubes.

Communication of information through intercellular nanotubes may develop between the same or different species growing on solid surfaces. These tubes enable acquisition of characteristics in a non-hereditary fashion



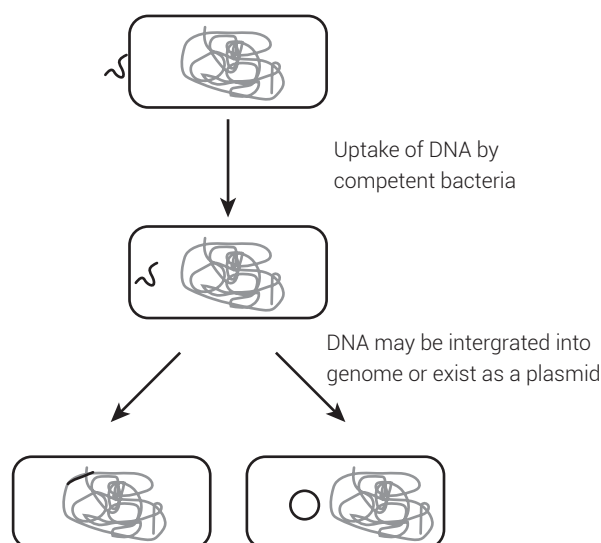
**Figure 2.** Bacterial conjugation where a thin tube (pilus) formed between the cells allows exchange of heritable information

so that antibiotic resistance becomes a temporary feature of the recipient bacterium. Some plasmids (extrachromosomal DNA material) may be transferred reciprocally.<sup>37</sup> Outer membrane vesicles produced by bacteria may also facilitate delivery of proteins and DNA and RNA between bacterial strains.<sup>38</sup>

Horizontal gene transfer can transform normally harmless bacteria into disease-causing ones. Indeed, it appears that the majority of genes for pathogenicity moving across taxa are acquired through bacterial viruses via transduction.<sup>11</sup> These phages may stimulate toxin production, allow cell adherence to host tissues, allow host defences to be evaded, and may stimulate genes to replicate and transduce.<sup>39</sup> The classic example of conversion of a non-disease-causing bacterium to a pathogen is *Corynebacterium diphtheria*.<sup>40</sup> Acquiring a phage carrying the structural gene for exotoxin production enables it to become pathogenic.<sup>41</sup>

Genes for exotoxins can be carried by plasmids and phages. New pathogens may arise following the transduction of a toxin gene from some environmental source to a member of the normal human microbiota. For example, *Staphylococcus aureus* may have acquired its exotoxin gene from the environmental bacterium *Pseudomonas* (> 95% similar) via a phage.<sup>42</sup> Furthermore, genes responsible for pathogenic ability in *Corynebacterium* (*dtx*), *Shigella* (*stx*), and *Vibrio* (*ctx*) are present in environmental samples, and additional sources of the *Staphylococcus* exotoxin-like gene have been found there as well. Phages isolated from the environment (water, sediment, and soil) would have carried all but the *dtx* gene. Conceivably, the genes would have functioned in the environmental bacteria to maintain homeostasis. There are indications that complex interactions also can occur among phages. These have enabled wild type and defective non-pathogenic *Vibrio cholera* to become pathogenic.<sup>43</sup> In the soil environment there exists a wealth of phage types with their numbers paralleling trends in bacterial populations.<sup>44</sup> Phage-bacterium and interphage interactions occur in the natural environment. This allows





**Figure 3.** Schematic view illustrating the uptake of naked DNA into a bacterial cell and its integration into the chromosome (left) or its circularisation to form a plasmid (right)

the construction of a coherent hypothesis for the emergence of pathogenic organisms.

An example of information transfer from an environmental bacterium is suggested from a study of non-pathogenic *Escherichia coli* isolates. Some of these carry a suite of genes enabling efficient iron uptake, such as the yersiniabactin system, which confers ecological fitness. When similar genes are present in *Yersinia* they contribute to pathogenic ability.<sup>45</sup> The transfer of the pathogenicity island is thought to be facilitated by a conjugative plasmid which has a wide host range.<sup>46</sup>

Other horizontal gene-transfer phenomena are known. Few credible suggestions exist to explain the gene acquisition noted among some organisms.<sup>47</sup> There are formidable restriction enzymes and other barriers to transformation among some bacteria and cyanobacteria. Some strains may lack these barriers, thus permitting transformation (figure 3).<sup>48</sup> In other instances, stress factors override the constraints normally experienced.<sup>49</sup> Additional sources of the genetic information transfer include the following:

a. Transfer of secretion-system capabilities among bacteria and beyond. Evidence suggests that the type III secretion proteins, widely present among plant and animal Gram negative bacteria, have been acquired through horizontal gene transfer from donor bacteria. Transfer also is postulated to occur in organisms that range from bacteria to protozoa. These secretion proteins facilitate pathogenic and mutualistic modes of existence. Many pathogenic bacteria use such a secretion system, which allows proteins to enter eukaryotic cells. This secretion system has similarities to components required for the

biosynthesis of flagella and other operational features noted in mutualist rhizobial bacteria.<sup>50</sup> These similarities suggest either transfer of capabilities among organisms or experimental manipulation by intelligent agents.

b. Bacterium-to-plant transfer. The bacterium *Agrobacterium tumefaciens* transfers genes from a plasmid (T-plasmid) to selected dicotyledonous plants, where they integrate naturally with the plant nuclear DNA and subsequently cause tumour formation. Tumours form as a consequence of auxin and cytokine production and the synthesis of supporting nutrients (opines) by the genes transferred.<sup>51</sup>

c. Plant-to-bacterium transfer. Genetic information acquired by bacteria may involve sources outside the prokaryotes. Information may come from decaying plants in the natural environment. For example, marker genes associated with chloroplast DNA present in residues of tobacco plants colonizing by the pathogenic bacterium *Ralstonia solanacearum* are transmissible to soil bacteria. More significantly, plant chloroplast DNA sequences were shown in 8% of bacteria growing on the residue. In the same environment *Acinetobacter* and *Pseudomonas* acquired exogenous plasmid DNA by transformation. Even without the presence of the plant pathogenic *Ralstonia*, *Acinetobacter* is able to transform on decaying tissues.<sup>52</sup> These studies raise the possibility of significant transfer of genetic information in soil and plant environments. Such transfer of information should not surprise as chloroplast DNA has many features similar to prokaryote DNA.<sup>53</sup>

Another intriguing illustration is provided by the pathogen *Xanthomonas axonopodis*. It causes a disease of citrus trees characterized by the appearance of wet lesions. The bacterium contains a gene sequence that encodes a protein able to influence the capacity of the plant to take ions and water into cells. It has a high degree of similarity with a sequence in the plant that encodes a plant natriuretic peptide. This protein maintains homeostasis when the plant is subjected to osmotic stress. Evidence suggests that the gene was acquired by the bacterium through horizontal gene transfer from the plants. This allows the bacterium to induce plants to increase uptake of ions and water into cells, which favours the growth and survival of the bacterium in plant tissues.<sup>54</sup> The acquisition of information from the plant may have been via similar mechanisms as discussed in the previous paragraph.

The basic assumption made in many research studies is that if a gene sequence shows greater similarity to those held by distantly related organisms than that by close relatives, it has the possibility of being an acquired gene.<sup>55</sup> It may be argued in some circumstances that similarity in DNA signature strongly suggests the existence of a Designer. The complexity of inferences that can be made from data

means that a number of lines of evidence need to converge before horizontal transfer can be asserted to have occurred with confidence.<sup>56</sup>

## Conclusions

Several fundamental changes following the Fall are indicated in Genesis and Job. Many of the changes associated with the emergence of pathogenic bacteria from non-pathogenic ones can be accounted for by naturalistic phenomena. However, the possibility remains that intelligent agents may have manipulated the genetic material.

There is evidence for alteration in the gene regulatory network (mutations and other phenomena) in the presence of stress, particularly the non-coding region of the chromosome. As a consequence, feedback processes, dominant metabolic pathways, and other aspects of cellular function can be changed in the host or microbe. Evidence has been presented for the exchange of information among mutualists, endosymbionts, and saprophytic bacteria with the occasional help of bacterial viruses and accession of DNA from other organisms. Gene loss enabling the expression of pathogenic ability has been responsible for the emergence of some pathogens, and it also appears that changes in the host genome have allowed opportunistic organisms to become pathogenic. Environmental stressors have facilitated the appearance of pathogens. Ostensibly, the massive increases in decaying organic debris available following the Fall, with the associated release of DNA into the environment, has played a role in the changes I have sought to explain.

## References

- Bergman, J., Did God make pathogenic viruses? *J. Creation* **13**(1):115–125, 1999; Francis, J.W., The organosubstrate of life: a creationist perspective of microbes and viruses, *Proceedings of the Fifth International Conference on Creationism*, pp. 433–444, 2003, [www.answersingenesis.org/articles/aid/v4/n1/organosubstrate-of-life](http://www.answersingenesis.org/articles/aid/v4/n1/organosubstrate-of-life).
- Rana, F., Did God create flesh-eating bacteria? A creation model for the origin of human disease, *Reasons to Believe*, 2010, [www.reasons.org/articles/did-god-create-flesh-eating-bacteria-a-creation-model-for-the-origin-of-human-disease](http://www.reasons.org/articles/did-god-create-flesh-eating-bacteria-a-creation-model-for-the-origin-of-human-disease).
- Borger, P., Evidence for the design of life: part 2—Baranomes, *J. Creation* **22**(3): 68–76, 2008; Borger, P., The design of life: part 4—variation-inducing genetic elements and their function, *J. Creation* **23**(1):107–114, 2009.
- Wood, T.C., The Ageing process: rapid post-flood intrabaraminic diversification caused by altruistic genetic elements (AGES), *Origins* **54**:5–34, 2002.
- Gillen, A., Microbes and the days of creation, *Answers Research J.* **1**:7–10, 2008; Shipton, W.A., Thorns also and thistles, *J. Adventist Theological Society* **23**(1):18–45, 2012.
- David, R., Microbiome: pathogens and commensals fight it out, *Nature Reviews Microbiology* **10**:445, 2012 | doi:10.1038/nrmicro2818.
- Sokurenko, E.V., Hasty, D.L. and Dykhuizen, D.E., Postadaptive mutations: gene loss and variation in bacterial pathogens, *Trends in Microbiology* **7**(5):191–195, 1999.
- MacNeil, L.T. and Walbourn, A.J.M., Gene regulatory networks and the role of robustness and stochasticity in the control of gene expression, *Genome Research* **21**(5):645–657, 2011.
- Climate change after sin is inferred by reference to Genesis 3:21. Moving from no clothes to animal skin coverings to maintain comfort may suggest this; Arnold, D.L., Jackson, R.W., Waterfield, N.R. *et al.*, Evolution of microbial virulence: the benefits of stress, *Trends in Genetics* **23**(6):293–300, 2007; Beck, M.A., Nutritionally induced oxidative stress: effect on viral disease 1'2'3, *American J. Clinical Nutrition* **71**(6):1676s–1679s, 2000.
- MacNeil, L.T. and Walbourn, A.J.M., Gene regulatory networks and the role of robustness and stochasticity in the control of gene expression, *Genome Research* **21**(5):645–657, 2011.
- Gal-Mor, O. and Finlay, B.B., Pathogenicity islands: molecular toolbox for bacterial virulence, *Cellular Microbiology* **8**(11):1707–1719, 2006.
- Somatic hypermutation represents a special category as the process contains highly sophisticated elements and the effects are limited to a single cell—cf. Peled, J.U., Kuang, F.L., Iglesias-Ussel, M.D. *et al.*, The biochemistry of somatic hypermutation, *Annual Review of Immunology* **26**:481–511, 2008.
- Casadevall, A. and Pirofski, L., Host–pathogen interactions: redefining the basic concepts of virulence and pathogenicity, *Infection and Immunity* **67**(8):3703–3713, 1999; Casadevall, A. and Pirofski, L., Host–pathogen interactions: the attributes of virulence, *J. Infectious Diseases* **184**(3):337–344, 2001.
- Vulić, M., Lenski, R.E. and Radman, M., Mutation, recombination, and incipient speciation of bacteria in the laboratory, *Proceedings of the National Academy of Sciences USA* **96**(13):7348–7351, 1999; Willey, J.M., Sherwood, L.M. and Woolverton, C.J., *Prescott's Microbiology*, 8<sup>th</sup> edition, McGraw Hill, New York, pp. 371–374, 2011.
- Schubert, S., Picard, B., Gouriou, S. *et al.*, *Yersinia* high-pathogenicity island contributes to virulence in *Escherichia coli* causing extraintestinal infections, *Infection and Immunity* **70**(9):5335–5337, 2002.
- Casadesús, J. and Low, D.A., Epigenetic gene regulation in the bacterial world, *Microbiology and Molecular Biology Reviews* **70**(3):830–856, 2006; Low, D.A. and Casadesús, J., Clocks and switches: bacterial gene regulation by DNA adenine methylation, *Current Opinion in Microbiology* **11**(2):106–112, 2008.
- Kasuga, T. and Gijzen, M., Epigenetics and the evolution of virulence, *Trends in Microbiology* **21**(11):575–582, 2013.
- Gándara, B., Merino, A.L. and Martínez-Romero, E., Limited genetic diversity of *Brucella* spp., *J. Clinical Microbiology* **39**(1):235–240, 2001; Martínez, M., Ugalde, R. A. and Almirón, M., Dimeric *Brucella abortus* Irr protein controls its own expression and binds haem, *Microbiology* **151**:3427–3433, 2005.
- Freiberg, C., Fellay, R., Bairoch, A. *et al.*, Molecular basis of symbiosis between *Rhizobium* and legumes, *Nature* **387**(6631):394–401, 1997.
- Dunning Hotopp, J.C., Clark, M.E., Oliveira, D.C.S.G. *et al.*, Widespread lateral gene transfer from intracellular bacteria to multicellular eukaryotes, *Science* **317**(5845):1753–1756, 2007.
- Foster, J., Ganatra, M., Kamal, I. *et al.*, The *Wolbachia* genome of *Brugia malayi*: endosymbiont evolution within a human pathogenic nematode, *PloS Biology* **3**(4):e121, 2005, doi: 10.1371/journal.pbio.0030121.
- Bian, G., Joshi, D., Dong, Y. *et al.*, *Wolbachia* invades *Anopheles stephensi* populations and induces refractoriness to *Plasmodium* infection, *Science* **340**(6133):748–751, 2013.
- Gnanamanickam, S.S. (Ed.), *Plant-associated Bacteria*, Springer, Dordrecht, Netherlands, 2007.
- Killham, K., *Soil Ecology*, University of Cambridge Press, Cambridge, p. 44, 2001.
- Shipton, W.A., *The Biology of Fungi Impacting Human Health*, Trafford Publishing, Singapore, pp. 3, 150–151, 2012.
- Irlinger, F., Safety assessment of dairy microorganisms: coagulase-negative staphylococci, *International J. Food Microbiology* **126**(3):302–310, 2008.
- Jensen, G.B., Hansen, B.M., Eilenberg, J. *et al.*, The hidden lifestyles of *Bacillus cereus* and relatives, *Environmental Microbiology* **5**(8):631–640, 2003.
- Ezpechuk, Y.V., Biology of pathogenicity (theoretical review), *Annual Review and Research in Biology* **3**(4):805–813, 2013; Klee, S.R., Brzuszkiewicz, E.B., Nattermann, H. *et al.*, The genome of *Bacillus* isolate causing anthrax in chimpanzees combines chromosomal properties of *B. cereus* and *B. anthracis* virulence plasmids, *PloS One*, 9 July 2010 | doi: 10.1371/journal.pone.0010986; Luna, V.A., King, D.S., Peak, K.K. *et al.*, *Bacillus anthracis* virulent plasmid pX02 genes found in large plasmids of two other *Bacillus* species, *J. Clinical Microbiology* **44**(7):2367–2377, 2006; Makino, S., Uchida, I., Terakado, N. *et al.*, Molecular characterization and protein analysis of the cap region, which is essential for encapsulation in *Bacillus anthracis*, *J. Bacteriology* **171**(2):722–730, 1989.

29. Maurelli, A.T., Fernandez, R.E., Bloch, C.A. *et al.*, “Black holes” and bacterial pathogenicity: a large genomic deletion that enhances the virulence of *Shigella* spp. and enteroinvasive *Escherichia coli*, *Proceedings of the National Academy of Sciences USA* **95**(7):3943–3948, 1998.
30. Freitag, N.E., Port, G.C. and Miner, M.D., *Listeria monocytogenes*—from saprophyte to intracellular pathogen, *Nature Reviews Microbiology* **7**(9):623–628, 2009.
31. Vento, S., Cainelli, F. and Temesgen, Z., Lung infections after cancer chemotherapy, *Lancet Oncology* **9**(10):982–992, 2008.
32. Silva, I.N., Tavares, A.C., Ferreira, A.S. *et al.*, Stress conditions triggering mucoid morphotype variation in *Burkholderia* species and effect on virulence in *Galleria mellonella* and biofilm formation in vitro, *PloS One*, 16 December 2013 | doi:10.1371/journal.pone.0082522.
33. Cox, E.C., Recombination, mutation and the origin of species, *BioEssays* **17**(9):747–749, 1995; LeClerc, J.E., Li, B., Payne, W.L. *et al.*, High mutation frequencies among *Escherichia coli* and *Salmonella* pathogens, *Science* **274**(5290):1208–1211, 1996.
34. Donnenberg, M.S. and Whittam, T.S., Pathogenesis and evolution of virulence in enteropathogenic and enterohemorrhagic *Escherichia coli*, *J. Clinical Investigation* **107**(5):539–548, 2001.
35. Bailey, K.L., Wyatt, T.A., Romberger, D.J. *et al.*, Alcohol functionally upregulates Toll-like receptor 2 in airway epithelial cells, *Alcoholism, Clinical and Experimental Research* **33**(3):499–504, 2009; Cangelosi, G.A., Ankenbauer, R.G. and Nester, E.W., Sugars induce the *Agrobacterium* virulence genes through periplasmic binding protein and a transmembrane signal protein, *Proceedings of the National Academy of Sciences USA* **87**(17):6708–6712, 1990; Fiester, S.E. and Actis, L.A., Stress responses in the opportunistic pathogen *Acinetobacter baumannii*, *Future Microbiology* **8**(3):353–365, 2013.
36. Subromoni, S., Nathoo, N., Klimov, E. *et al.*, *Agrobacterium tumefaciens* responses to plant-derived signalling molecules, *Frontiers in Plant Science* **5**:322, 2014 | doi:10.3389/fpls.2014.00322.
37. Dubey, G.P. and Ben-Yehuda, S., Intercellular nanotubes mediate bacterial communication, *Cell* **144**(4):590–600, 2011.
38. Fulsundar, S., Harms, K., Flaten, G.E. *et al.*, Gene transfer potential of outer membrane vesicles of *Acinetobacter baylyi* and effects of stress on vesiculation, *Applied and Environmental Microbiology* **80**(11):3469–3483, 2014; Hasegawa, Y., Futamata, H. and Tashiro, Y., Complexities of cell-to-cell communication through membrane vesicles: implications for selective interaction of membrane vesicles with microbial cells, *Frontiers in Microbiology* **6**:633, 2015 | doi:10.3389/fmicb.2015.00633; Mashburn-Warren, L.M. and Whiteley, M., Special delivery: vesicle trafficking in prokaryotes, *Molecular Microbiology* **61**(4):839–846, 2006.
39. Christie, G.E., Allison, H.E., Kuzio, J. *et al.*, Prophage-induced changes in cellular cytochemistry and virulence; in: Hyman, P. and Abedon, S.T. (Eds.), *Bacteriophages in Health and Disease*, CABI, Wallingford, UK, pp. 33–60, 2012; Kuhl, S., Abedon, S.T. and Hyman, P., Diseases caused by phages, in *Bacteriophages in Health and Disease*, pp. 21–32, 2012; Plata, K., Rosato, A.E. and Wegrzyn, G., *Staphylococcus aureus* as an infectious agent: overview of biochemistry and molecular genetics of its pathogenicity, *Acta Biochimica Polonica* **56**(4):597–612, 2009; Wagner, P.L. and Waldor, M.K., Bacteriophage control of bacterial virulence, *Infection and Immunity* **70**(8):3985–3993, 2002; Ziebuhr, W., Ohlsen, K., Karch, H. *et al.*, Evolution of bacterial pathogenesis, *Cellular and Molecular Life Sciences* **56**(9–10):719–728, 1999.
40. Freeman, V.J., Studies on the virulence of bacteriophage-infected strains of *Corynebacterium diphtheria*, *J. Bacteriology* **61**(6):675–688, 1951.
41. Uchida, T., Gill, D.M. and Pappenheimer, A.M., Mutation in the structural gene for diphtheria toxin carried by temperate phage  $\beta$ , *Nature, New Biology* **233**(35):8–11, 1971; Uchida, T., Pappenheimer, A.M. and Greany, R., Diphtheria toxin and related proteins. 1. Isolation and properties of mutant proteins serologically related to diphtheria toxin, *J. Biological Chemistry* **248**(11):3838–3844, 1973.
42. Casas, V., Magbanua, J., Sobrepeña, G. *et al.*, Reservoir of bacterial exotoxin genes in the environment, *International J. Microbiology* 2010, article ID 754368 | doi:10.1155/2010/754368.
43. Hassan, F., Kamruzzaman, M., Mekalanos, J.J. *et al.*, Satellite phage TLC  $\phi$  enables toxigenic conversion of CTX phage through *dif* site alteration, *Nature* **467**(7318):982–985, 2010.
44. Williamson, K.E., Soil phage ecology: abundance, distribution, and interactions with bacterial hosts; in: Witzany, G. (Ed.), *Biocommunication in Soil Microorganisms*, Springer, New York, pp. 113–136, 2011.
45. Hacker, J. and Kaper, J.B., Pathogenicity islands and the evolution of microbes, *Annual Review of Microbiology* **54**:641–679, 2000; Toh, H., Oshima, K., Toyoda, A. *et al.*, Complete genome sequence of the wild-type commensal *Escherichia coli* strain SE15, belonging to phylogenetic group B2, *J. Bacteriology* **192**(4):1165–1166, 2010.
46. Antonenka, U., Nölting, C., Heesemann, J. *et al.*, Horizontal transfer of *Yersinia* high-pathogenicity island by the conjugative RP4 *atrB* target-presenting shuttle plasmid, *Molecular Microbiology* **57**(3):727–734, 2005.
47. Gilbert, C., Schaack, S., Pace, J.K. *et al.*, A role for host–parasite interactions in the horizontal transfer of DNA transposons across animal phyla, *Nature* **464**(7293):1347–1350, 2010; Yue, J., Hu, X., Sun, H. *et al.*, Widespread impact of horizontal gene transfer on plant colonization of land, *Nature Communications* **3**, article 1152, 2012 | doi:10.1038/ncomms2148.
48. Corvaglia, A.R., Francois, P., Hernandez, D. *et al.*, A type III-like endonuclease functions as a major barrier to horizontal gene transfer in clinical *Staphylococcus aureus* strains, *Proceedings of the National Academy of Sciences USA* **107**(26):11954–11958, 2010; Stucken, K., Koch, R. and Dagan, T., Cyanobacterial defense mechanisms against foreign DNA transfer and their impact on genetic engineering, *Biological Research* **46**(4):373–382, 2013.
49. LeClerc, Li, Payne *et al.*, ref. 33.
50. Freiberg, C., Fellay, R., Bairoch, A. *et al.*, Molecular basis of symbiosis between *Rhizobium* and legumes, *Nature* **387**(6631):394–401, 1997; Brown, N.F. and Finlay, B.B., Potential origins and horizontal transfer of type III secretion systems and effectors, *Mobile Genetic Elements* **1**(2):118–121, 2011; Silva, D.C.F., Silva, R.C., Ferreira, R.C. *et al.*, Examining marginal sequence similarities between bacterial type III secretion systems and *Trypanosoma cruzi* surface proteins: horizontal gene transfer of convergent evolution, *Quantitative Biology, Populations and Evolution*, Cornell University, 2012, www.arxiv.org/abs/1211.6611v1.
51. de la Riva, G.A., González-Cabrera, J., Vázquez-Padrón, R. *et al.*, *Agrobacterium tumefaciens*: a natural tool for plant transformation, *EJB Electronic J. Biotechnology* **1**(3):118–133, 1998.
52. Monier, J.-M., Bernillon, D., Kay, E. *et al.*, Detection of potential transgenic plant DNA recipients among soil bacteria, *Environmental Biosafety Research* **6**(1–2):71–83, 2007; Pontiroli, A., Rizzi, A., Simonet, P. *et al.*, Visual evidence of horizontal gene transfer between plants and bacteria in the phytosphere of transplastomic tobacco, *Applied and Environmental Microbiology* **75**(10):3314–3122, 2009.
53. Hofkin, B.V., *Living in a Microbial World*, Garland Science, Taylor and Francis Group, LLC, New York, p. 211, 2011.
54. Nembaware, V., Seoighe, C., Sayed, M. *et al.*, A plant natriuretic peptide-like gene in the bacterial pathogen *Xanthomonas axonopodis* may induce hyperhydration in the plant host: a hypothesis of molecular mimicry, *BMC Evolutionary Biology* **4**:10, 2004 | doi:10.1186/1471-2148-4-10.
55. Yue, Hu, Sun *et al.*, ref. 47.
56. Schaack, S., Gilbert, C. and Feschotte, C., Promiscuous DNA: horizontal transfer of transposable elements and why it matters for eukaryotic evolution, *Trends in Ecology and Evolution* **25**(9):537–546, 2010.

**Warren A. Shipton** received his B.Sc.Agr. (hons) in 1961 and a Ph.D. from the University of Sydney and subsequently an M.Ed. from James Cook University. He has published extensively in the biological sciences, including biomedical science. He is a Fellow of the Australian Society for Microbiology. He has published widely in professional journals, has been a dean of science at James Cook University and president of Asia-Pacific International University, Thailand, where he still enjoys an active role in science.



# The overthrusting paradox: a challenge to uniformitarian geology and evolution

John D. Matthews

Overthrusting is regarded as a paradox by the geological community. The concept of overthrusting has been defined by secular motives rather than physics. However, the paradox disappears if geologists recognize that they have treated the geological column as immutable rather than empirical and therefore open to questioning. Since the geological column is a key pillar supporting evolution, Christians ought to actively re-engage in discussion about the column's validity.

Many geologists believe that overthrusting<sup>1</sup> has occurred in places where large blocks of 'older' rock overlie 'younger' rock. This unusual positioning of the older rock is therefore interpreted, not by a sedimentary event, but through massive physical movements, all of which are then judged to be paradoxical.<sup>2</sup> To unravel the paradox we need to:

1. examine the rationale for identifying overthrusting,
2. recheck the physics behind the proposed movement, and
3. show that a reasonable explanation for the origin of the overthrust rock and its pathway to its new location (palaeo-reconstruction) can be provided.

Little effort has gone into item 1. Most of the effort by uniformitarian geologists to resolve the paradox has focused on item 2, the physics. Many of the examples considered by uniformitarians merely reaffirm the paradox that the physical aspect of the overthrusting movement is impossible. In other cases, elaborate and often imaginative geochemical physical models, which will be shown to contain fundamental flaws, have been offered as explanations. Therefore, these do not make the overthrust paradox disappear. Item 3 has rarely been tackled. Our study shows that there is no effective way to achieve palaeo-reconstruction. Thus dilemmas with items 2 and 3 point to item 1 as the key to resolving the paradox. Identification of the 'overthrust' as a movement depends critically on the robustness of the geological column. Thus there are two key reasons to reject the column—the deep questions about the assumptions and motives behind its construction and the problem of overthrusting. We end with a call for Christians to engage more actively on discussions about the column because of its direct links to evolution.

## The rationale for identifying overthrusting

There are many places in the world where large blocks of 'older' rock overlie 'younger' strata. The belief that older rocks overlie younger rocks is based on the observed inconsistency with the expected stratigraphic order of either

rock facies or their fossils from the geological column,<sup>3</sup> metamorphic rock overlying 'country rock', or radiometric dates. This implies that the older rock was emplaced over the younger by a sliding movement.

There may be an interface layer between the lower younger layer and the upper older one which has rheological properties that could have aided overthrusting. However, it is circular reasoning to use this as proof of overthrusting. Such layers can exist within vertical sequences of rocks deemed to be undisturbed because they replicate the geological column.

Instances where a thrust is identified by metamorphic rock overlying country rocks are limited. And while creationists have suggested that radiometric dating can at least provide relative dating,<sup>4</sup> there are serious doubts.<sup>5</sup> There are instances where overthrusting has been identified by seismic sections and well-bore core analysis. In this short paper, the focus has to be on visible overthrusts. Mechanisms and explanations are not likely to be different elsewhere.

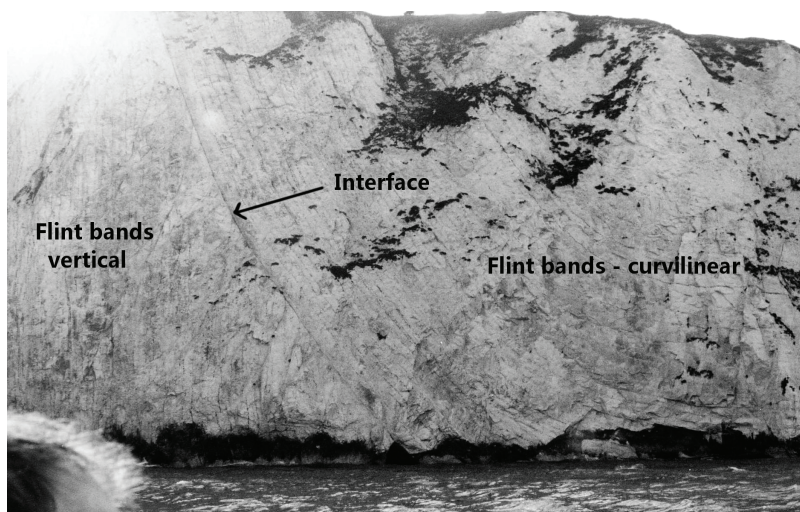
## The geological column

The history of the development of the geological column is complex,<sup>6</sup> but for convenience we identify three key stages. Giovanne Arduino, in 1759, proposed three divisions of Earth's rocks based primarily on rock type.<sup>7</sup> Later, the focus moved to identification by fossils with the geological mapping in the UK by William Smith.<sup>8</sup> In coal mining and canal construction (1795 onwards) he found what appeared to be similar vertical sequences of fossils across wide areas. Geologists in continental Europe were noting the same thing, so Arduino's classification of Primary–Secondary–Tertiary strata developed into a more sophisticated column. The column is now tightly defined with respect to fossils and radiometric dating by international committees of uniformitarians.<sup>9</sup> While some realise that it is shaky in places, there is a distinct unwillingness to undertake fundamental reviews.<sup>10</sup>

While localized correlations, as Smith noticed, may accurately demonstrate portions of the geological column, the worldwide correlation is purely hypothetical.<sup>11</sup> Our historical study of overthrusting shows that the column (and its template, which correlates the strata with the time of original deposition) is intimately bound up with the effects and attitudes, even on scientists, of the 18<sup>th</sup>-century ‘Enlightenment’. Dominated by French philosophers, but with support from countries like Germany and Scotland, their aims may be summarized by Charles Lyell’s words: “A class of writers ... had been laboring industriously for many years, to diminish the influence of the clergy, by sapping the foundations of the Christian faith.”<sup>12</sup> In private letters published after his death, we learn that he wanted to subvert the idea that the Mosaic texts had anything useful to say about geology.<sup>13</sup> Much the same attitude to the biblical Flood is shown by Arthur Holmes a century later—that the belief in the Noachian “Deluge ... obstruct[ed] the progress of geology”.<sup>14</sup> But his suggestion that Biblicalism obstructs geology is wrong.<sup>15</sup> Secular motives are not a good starting point for finding truth.

### The paradox

Attempts to explain the mechanics of ‘thrusting’ are legion.<sup>16–19</sup> However, many overthrusts remain paradoxical because “for a thrust sheet to overcome the shear resistance when moving along its base, higher stresses are required than the sheet can withstand”.<sup>20</sup> A solution is no nearer today than in 1991, when Price and Cosgrove wrote that studies are “openly or tacitly critical and contradictory”.<sup>17</sup> Tentative explanations have been offered for cases where the ‘overthrust’ block (apparently) slid downhill under gravitational forces, but these are a minor fraction of cases.<sup>21</sup>



**Figure 1.** Ballard Down Cliffs, showing the supposed ‘overthrust’ (Author’s photo, May 2002)

Horizontal and uphill overthrusting becomes more difficult to explain, since tractive effort is needed. Gravitational spreading, ‘caterpillaring’, and base contraction have been suggested, but there are doubts about these, and they only apply to a very limited class of overthrusts.<sup>18</sup>

### A specific overthrust, physics, and motives

As geological mapping moved from the eighteenth century to the nineteenth, contradictions appeared with the ‘Enlightenment’ desire to demonstrate a consistent worldwide ‘geological column’. Thomas Webster, said to have been a competent geologist,<sup>22</sup> spotted an unconformity at Ballard Down, Dorset, UK, in the chalk in 1812.

The curvilinear form of the rock ‘layering’ dies out to the north (figure 1, right side), and there is no change in fossil assemblages across the interface. The logic for identifying it as an unconformity is illustrated in the schematic (figure 2). The flint bands have been used to define a series of depositional layers since they follow the trends of other lithostrata outside the photographed area.

The interpretation is that ‘Cretaceous’ chalk was deposited in the south as a series of layers (1 to 8 (figure 2), and possibly others obscured beneath sea level) roughly horizontally over local ‘Jurassic’ strata. Subsequent progressive folding to the North while chalk sedimentation was still taking place resulted in new chalk layers (i to v (figure 2) eroding the hatched area and being distorted into that curvilinear shape while still in an unconsolidated state. It is therefore an unconformity because chalk layer i, which is younger than layers 1 to 8, progressively oversteps those older layers 8 back to 1.

This assessment of Ballard Down occurred at the time ‘The Enlightenment’ was making serious inroads into people’s attitudes to biblical history<sup>6</sup> and the feature was as much a battleground as it was an outcrop.<sup>6</sup> To avoid retreating from this new ‘enlightened’ worldview with its emerging geological column, Ballard Down was proclaimed a thrust in 1822.<sup>22</sup> If it had not been, uniformitarians would have had to admit that there was an unconformity in ‘Cretaceous’ deposits caused by a ‘Tertiary’ timed event which tilted layers 1 to 8 to the vertical.

Almost ten different rock mechanics and structural geological studies have appeared since 1822 trying to explain the feature as an ‘overthrust’. The latest was a discussion between those supporting a southern overthrust<sup>23,24</sup> and others supporting a northern underthrust.<sup>25</sup> There

was no reconciliation. Furthermore, the thrust interpretation implies a lateral movement of at least 100 m, implying a visible brecciation zone at least a metre thick.<sup>26</sup> Like other physical issues, its absence (see figure 1) seems to matter less than the preservation of the paradox. To uniformitarians, Ballard Down is a puzzle, whereas creationists have no reason to reject Webster's original interpretation of it being an unconformity.

### Creationists challenge overthrusting

By 1926, George McCready Price<sup>27</sup> had documented his view that overthrusting remained a paradox because of uniformitarian assumptions in their identification—our item 1. Davis Young, though a Christian and a geology professor, criticized Price and his argument.<sup>28</sup> He noted that Price was a self-taught geologist who wrote and communicated with sufficient sophistication to deceive many untrained in uniformitarian geology with his view that “the whole idea of overthrusting was devised by geologists simply to salvage the dogma of fossil succession”, and thus link it intimately with evolution.

But Young's critique falls short. Morris noted that Price was well trained in science and engineering.<sup>29</sup> Furthermore, Young's description of Price as an amateur geologist and good communicator could equally describe Sir Charles Lyell, who had launched the questionable uniformitarianism as part of his personal contribution to ‘The Enlightenment’, ridding science of its original Mosaic/biblical anchor.<sup>13</sup> Price objected to evolution and uniformitarian geology for many reasons, not just overthrusting. Young, an igneous petrologist, is not a stratigrapher either, and his attack on Price is essentially *ad hominem*.

In 1931, Byron Nelson addressed the overthrusting paradox,<sup>30</sup> as did John Whitcomb and Henry Morris (1961) in *The Genesis Flood*,<sup>31</sup> using the examples of the Heart Mountain and Lewis overthrusts. Photographs of the planes along which the rocks supposedly moved showed no significant breccia, which should be present.<sup>26</sup> But they also noted two significant problems:

1. Failure to provide a plausible palaeo-reconstruction. This is a significant problem for uniformitarian geology in the oil industry.<sup>15</sup> Chemical signatures are often used to suggest how different masses of rocks had a common origin,<sup>32</sup> but typically ignore palaeo-reconstruction. Potentially

this is due to the failure to consider that sediments were sourced directly from the fountains of the great deep in an episodic manner (as Genesis 7:11 implies) rather than to only consider them as erosional products from topographic highs as part of a Davisian cycle;

2. No mechanical solution for such movements has been demonstrated.

Uniformitarian geologists have attempted to explain large movements, like that of Heart Mountain, which Young<sup>28</sup> used, to oppose the Flood paradigm. But even assuming that the Heart Mountain block slid downhill (discussed and rebutted below), there are other serious problems. Even those geologists not willing to use the word ‘paradox’ still recognize its problematic nature.<sup>17,33</sup>

Many more overthrusts have been described by both creationist authors<sup>34</sup> and uniformitarian Murrell,<sup>18</sup> the latter of whom mentions the well-known Glarus and Lewis thrusts. He notes the significant distances moved and the dimensions of the blocks. Movements have exceeded 80 km, and block sizes have exceeded 170 km. So if ‘older’ rock came to rest on ‘younger’ rock, explaining how is not trivial.

### The reluctance to challenge the geological column

We can understand the motives of uniformitarians not to challenge the geological column—the theory of evolution is at stake. But what is the problem for Christians? Some creationists accept the column as an observational fact (e.g. Garner,<sup>35</sup> Snelling,<sup>36</sup> and Tyler<sup>37</sup>). They accept the same fossil order as evolutionists do, but they do not believe the fossil order substantiates evolution. An appeal is typically made to a concept called the ‘Law of Faunal Succession’

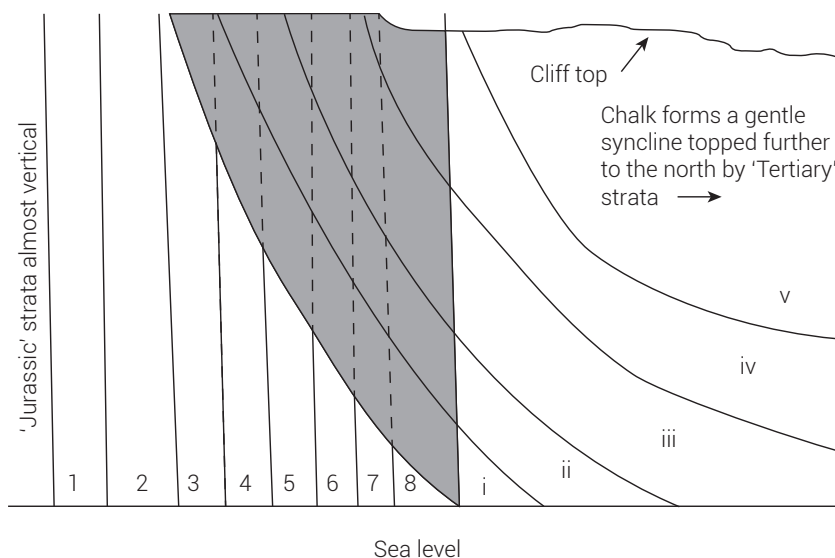
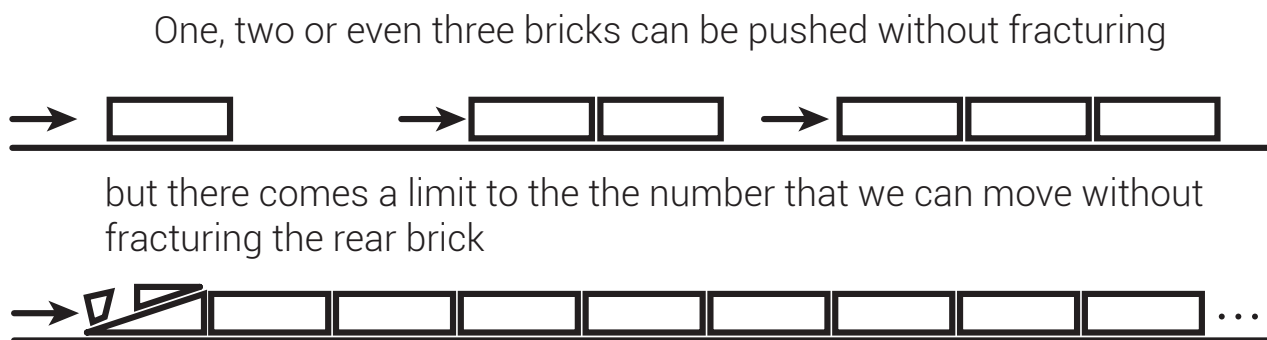


Figure 2. The layering of the chalk deposits across the unconformity





**Figure 3.** An Illustration of the problems of overthrusting using household bricks

to explain localized correlations. But against observational challenges to the geological column, such as in this paper and elsewhere, such creationists will always struggle to explain the law in its local and the more problematical continent-wide correlation. We have no independent record of the number or the locations of the Fountains of the Great Deep, which caused the burial environments or the pre-Flood ecological distribution of living creatures that ended up as fossils. Only those would provide a starting point to justify further discussion on the subject, so the ‘law’ remains merely an *en passant* idea.

Aside from numerous creationists who accept the column, there are many influential Christians who insist that evolution is true because of the geological column. These include Dr Denis Alexander, a biologist and past editor of *Science and Christian Belief*. He is a prolific author<sup>38,39</sup> and believes that evolution is demonstrated by the rocks. He claims that any examples of out-of-order fossils would appear in ‘mainstream’ journals,<sup>39</sup> but ignores the explicit embargo on such material, like that of the 2008 statement by The Geological Society, London<sup>40</sup> or the Royal Society that insists the earth is very old, evolution took place, and is supported by the fossil record. They affirm Gould’s NOMA solution, separating religion and science,<sup>41</sup> in contradistinction to St Paul’s claim (Romans 1:20) that they cannot be put into separate compartments. But debate on the subject is not the Society’s forte.<sup>42</sup> One of Alexander’s books, with co-author Professor Bob White,<sup>43</sup> is cited by the Society in support of this deliberate separation.

Other Christians taking the same position include Professor R.J. (Sam) Berry,<sup>44</sup> who insists that “fossils demonstrate that the earth goes through major changes and long ages”. He and others do not engage with published critiques of his arguments which have long been discussed in *Journal of Creation*.<sup>45</sup> Professor Simon Conway Morris (evolutionary palaeobiologist) stated that “the fact of organic evolution itself is not in dispute. ... the fossil record ... seems to be unanswerably correct”.<sup>46</sup> There are many others.<sup>47–51</sup>

### The physics offered to explain thrusting

If there is reluctance to re-examine the geological column, we need to look more closely at the physics of the movements—our item 2. Readers are referred to classic papers for the detailed mathematics.<sup>17–19</sup>

Mechanical problems with large thrust blocks can be illustrated by using common bricks. If we place one brick on a flat surface, we can move it with ease (figure 3). If we place a second brick in front of the first, the force needed to move both doubles. Adding more bricks increases the necessary force proportionately. When the line of bricks is 10 km long (and depending on the quality of bricks, coefficient of friction, etc.), the rearmost bricks will begin to undergo micro-fracturing. With more bricks added up front, the rear bricks will eventually fail, with fractures at about 40° to the horizon.

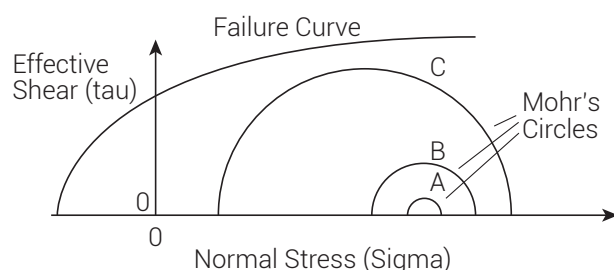
Figure 4 explains this phenomenon. The upper curve (the Coulomb failure curve) represents the strength (bearable shear) of the brick and increases with the vertical (lateral) compression applied. The internal forces in the brick are represented by the hemispheres (Mohr’s curves). When only a few bricks are being pushed, the hemisphere is small (curve A). With more bricks, it grows in size (curves B and C). With even more bricks, the hemisphere intersects the failure curve, and the back brick fractures.

Substituting a large block of rock for the bricks, we find that only a relatively short length of rock (compared to observed overthrust dimensions quoted above) can be moved without internal failure. This was known over 100 years ago by uniformitarian geologists.<sup>2</sup> The tractive force needed to overcome friction was judged to be the main restraining factor, and little attention was paid to cohesion. If we cement a single brick to the surface, the force needed to move the brick increases enormously. Under enough force, the brick and cement fracture in an erratic fashion. But strata do not usually merely rest on each other. Rocks are bound by

cements. Overcoming both friction and cohesion requires a smooth, clean sliding surface to avoid erratic fracturing.

We can use the equations developed by Jaeger *et al.*<sup>33</sup> to calculate the maximum lengths of overthrusts. Using common parameters, strength ( $C_0$ ) = 200 MPa, internal sliding friction ( $p$ ) = 0.1, cohesion ( $S$ ) = 50 MPa, friction ( $\mu$ ) = 0.6, and density 2,800 kg/m<sup>3</sup>, those lengths are shown in table 1. If cohesion is not a factor, it is possible to explain how overthrust-rocks may have been pushed moderate distances, but these are fractions of ‘reality’. When cohesion is factored in, the distances are insignificant.

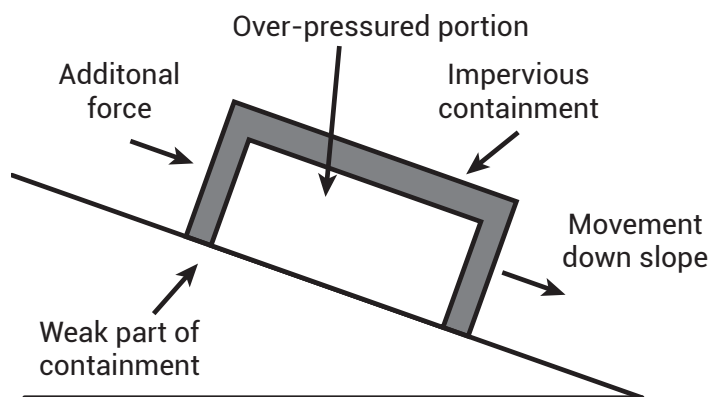
Many ideas have been floated to explain the ‘observed’ greater movement by thrust blocks. These focus on decreasing the frictional coefficient at the sliding surface,



**Figure 4.** The Coulomb-Mohr representation of a rock under stress and shear

**Table 1.** Lengths of blocks that could be moved without fracturing

Height (m)	Household bricks (0.06m)	1	10	100	1,000
<b>Without cohesion</b>					
Length horizontal	12.1 km	12.1 km	12.1km	12.2 km	12.2 km
Length (15 degrees uphill)	8.4 km	8.4 km	8.4 km	8.4 km	8.4 km
<b>With cohesion</b>					
Length horizontal	0.24 m	4 m	40 m	385 m	3.0 km
Length (15 degrees uphill)		4 m	40 m	380 m	2.7 km



**Figure 5.** Murrell's illustration for overthrusting of an overpressured block

typically using lubrication by water. But none applies on a wide scale in the field.

### Alleviation by overpressure?

Overpressured strata, found when drilling for hydrocarbons, are an observational fact. Instead of following a normal pressure gradient with depth (~10 MPa/km or ~0.44 psi/ft), overpressured rocks exhibit sharp increases in pressure.<sup>52</sup> The maximum is 2.3 times that of normal, which is equivalent to supporting the lithostatic load back to surface. Hubbert and Rubey<sup>19</sup> suggested that such an overpressured porous rock could effectively ‘float’ above the substrate, enabling large-scale thrusting. There are ten major problems which they did not address, and after another 65 years, uniformitarian comments on these are still absent.

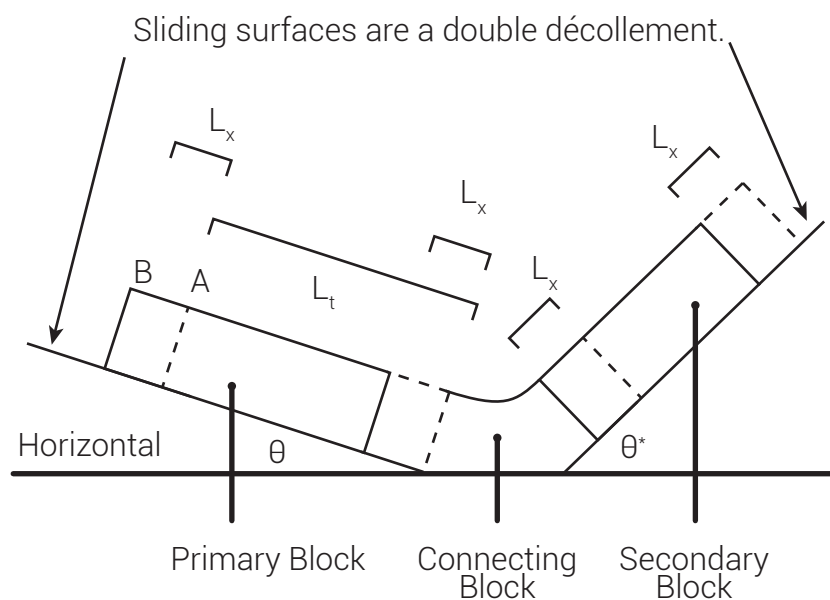
First, although observed overpressure values in the field range as high as 92% of the maximum, they are more typically around 60%,<sup>53</sup> so even granting an overpressured block, significant force is still needed.

Second, overpressure situations affect the rock mechanics. The strain hemisphere (cf. circle C in figure 4) moves to the left and increases in radius, bringing it closer to the failure curve.<sup>33</sup>

Third, geologists cannot explain how an overpressured condition at the sliding surface could be maintained once the block detaches from the location where it was deposited. Uniformitarian Murrell<sup>18</sup> recognizes the problem and wraps the block that is supposed to be moving with impervious rock (his figure 1). This is shown in figure 5 in simplified form. How did such a convenient wrapping arise? It is certainly not a characteristic of overpressured regions in the North Sea. The largest regions are small compared with what we have to explain.<sup>52</sup> It is another ignored aspect of palaeo-reconstruction.

Fourth, the amount of impervious rock needed has not been assessed, nor its effects. That requires an assessment of the strength of the cuboid container, with the weakest part being at the edges. Finite element methods could be used, but as an alternative we can simplify the mathematical challenge by changing the geometry.

Suppose we consider the sliding of an upright cylinder of overpressured rock surrounded by an annulus of strong impervious rock. We now have a one-dimensional tractable problem. Other



The Primary Block of length  $L_t$  and the Secondary Block both move a distance  $L_x$  from the dashed positions to the solid line positions.

In the process, the front of the overthrust block has moved from A to B.

Furthermore, the necessary physical properties of the connecting block bear no resemblance to any known rock.

**Figure 6.** Palaeo-reconstruction of overthrusting

equations in Jaeger *et al.*<sup>33</sup> allow us to compute the amount of impervious rock needed to meet the hoop stresses from the overpressure (and a cylindrical shape minimizes the amount of extra rock). The result is a 16-fold increase in mass using the listed rock properties. This extra mass does not ‘float’ on the substrate. It is ‘dead-weight’ and moving it without fracturing is impossible. Murrell’s<sup>17</sup> more realistic admission shown in figure 5 must require an even greater ratio of impervious rock than in our minimal example.

Fifth, even if the duplex block ever existed, how did the wrapper disappear without a trace being left?

Sixth, toe and heel effects have been ignored.<sup>2</sup> Figure 1 shows the ‘toe-problem’ at Ballard Down—the bending of the strata. This typically quadruples the force needed for movement, and decreases the amount of motion.<sup>2</sup> In the case of Ballard Down, plastic deformation of strata would have been possible if the chalk were not lithified, but if 30 million years had passed before the movement took place, it would by then have been lithified, and deformation would be a problem.

Seventh, reservoirs that are overpressured are generally weaker because they were buried rapidly and were not able to expel sufficient pore fluids to dewater completely. If it is hard to push a solid block of rock, how is it possible to push one that can plastically deform internally rather than slide across a décollement?

Eighth, non-porous rocks have been overthrust.

Ninth, studies have shown that overpressured conditions could not persist in crustal materials for more than 10,000 years.<sup>54</sup>

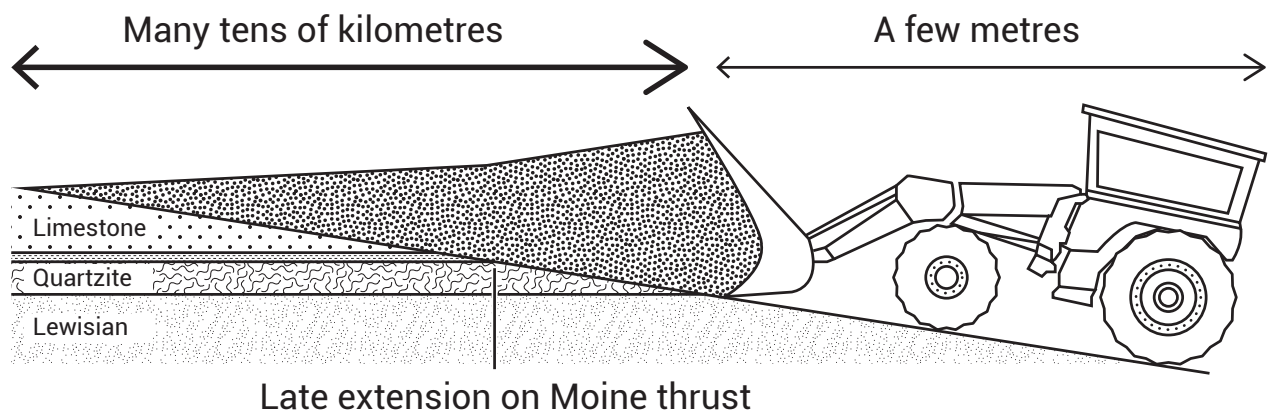
Tenth, how did the overpressures arise? Mainstream literature suggests that they arise from hydrocarbon generation.<sup>52</sup> But there is evidence that hydrocarbons cannot be formed under such suggested conditions and must have existed before the sedimentary events.<sup>15</sup> A uniformitarian fall-back suggestion is that of rapid sedimentation and loading, but such geologists won’t acknowledge that as evidence for The Flood.

### Palaeo-reconstruction—our item 3)

Thrusts require a base, a block to be moved—the *primary block*—and often another block to push the primary block—the *secondary block*. To move the primary block horizontally or uphill requires a push from the secondary block moving under the force of gravity and in contact with the primary block. To maintain contact between the two blocks during thrusting, a third block connecting them is required, length of which must be at least that of the translation of the primary block (figure 6). If the initial movement of the secondary block is downhill, then its ability to push is lost once it reaches a horizontal plane or uphill slope, and it will add to the frictional resistance of any movement.

Figure 6 shows that a primary block of length  $L_x$  sits on the substrate with an assumed angle  $\theta$ . During overthrusting





**Figure 7.** Trewin's explanation for the Moine overthrust

it moves a distance  $L_1$  so that the leading face moves from position A to position B. The secondary block, aligned in a downward direction (angle  $\theta^*$ ), also must move a similar distance.

As the primary block moves, the space vacated by its rear edge must be replaced by other rock, otherwise the force of the secondary block can no longer be transferred, and sliding will stop. Also, the compressive strength of all blocks must be greater than their failure force. The effective distance of thrusting is controlled by these factors. Any palaeo-reconstruction of thrusting must account for all of these factors. They limit both the size of the blocks and the distances that can be moved compared with the results in table 1; both are fractions of field interpretations.

There are two other problems in performing a viable palaeo-reconstruction. The required height of the secondary block is greater than observed field data. Based on angles ( $\theta^*$ ) of  $30^\circ$ – $60^\circ$  and linear lengths of 200 km, the secondary block would require a height between 100 and 200 km. Mount Everest is only 8.8 km high! Some uniformitarians recognize this problem.<sup>17</sup> In addition, any connecting block would have to behave in a plastic manner to accommodate the slope change, yet such consistency would prevent it from translating force. Furthermore, no such rock has been observed near thrusts.

### Other 'overthrust' examples

#### Glarus, Switzerland

The out-of-order strata at Glarus was probably the first major documented 'overthrust'. In 1840, Arnold Escher noted that Permo-Triassic strata overlay Cretaceous and Jurassic rocks. But, clearly unsure of his interpretation, did not publish his findings until 1849, and even then only

after consulting Roderick Murchison.<sup>55</sup> In the conflict between physical field data and the template of the emerging geological column, they chose the latter, and inferred that the Permo-Triassic strata (which, because it is a double-barrelled term, is a euphemism since the rocks are strictly 'undifferentiated') had been moved over the Jurassic and Cretaceous strata. Like Ballard Down, motives dominated and the desired explanation trumped data.

#### Moine, Scotland, UK

Northwest Scotland possesses a wide range of overthrusts.<sup>56</sup> The most significant is that at Moine, which is considered by many geologists to be similar to thrusts found in the Appalachians and Canadian Rockies. Many of these are not outcrops, but inferred from seismic and oil wells.

Moine illustrates uphill movement (about  $15^\circ$ ), and shows metamorphic rock overlying unmetamorphosed strata. Metamorphic rock is thought to be former 'country rock' exposed to extremes of heat and/or pressure. The thrust is also identified by biostratigraphy and radiometric dating. Geologists propose that the metamorphic rock slid from a distant location since any metamorphism afterwards would have affected the underlying rock. This interpretation was introduced in 1861.

Like Ballard Down, there have been numerous studies of the mechanics of the Moine thrust. Johnson and Mykura<sup>57</sup> note that this (paradoxical) overthrust "still presents considerable problems". These include the uphill motion and the presence of additional strata on top of the primary block. Worse, some of these piggy-backed strata are also out of order.

Trewin<sup>58</sup> offers a simple diagram (his fig. 4.48), redrawn as figure 7, to show how the Moine overthrust occurred. In his illustration, a bulldozer pushes the overthrust block up the slope. This misrepresents the force required. The block

would require the force of a million bulldozers behind each other every two metres. As noted earlier, such forces are difficult to generate and must still be lower than the failure strength of the rocks. Figure 7 reinforces the paradigm of sliding/overthrusting in a dishonest way. Furthermore, the ‘overthrust’ is said to have moved the visible block by 100 km.<sup>59</sup> Our mechanical analysis shows that this is not possible, even if we reduce the cohesion and friction to zero, since the maximum length of the block and its displacement cannot exceed 27 km for any practical thickness known in the area.

Other field data suggest Moine is no overthrust because the sequence of strata there is not a simple case of metamorphic rock overlying unmetamorphosed rock. Geological maps of the area show that a complex mixture of erosion, non-deposition and overthrusting would have been required to achieve the present configuration as interpreted by the geological column. Keeping the column violates Occam’s razor. We prefer to believe that minimizing assumptions yields a better approach, since basic faulting during emplacement could explain the data when the timing constraints associated with the geological column are removed. In addition, this suggests that metamorphic rock can form apart from heat.

#### Heart Mountain

The Heart Mountain thrust (or detachment) is significant because of its size. It has been the subject of many studies in the past 50 years, perhaps impelled by its use in *The Genesis Flood* and the desire to rebut the Flood paradigm and continue to live in the secular ‘Enlightenment’.

Recent theories propose that the release of carbon dioxide at the detachment surface provided a cushion, allowing the blocks to ‘float’ down a two-degree slope, even though the natural coefficient of friction at  $\sim 0.6$  would still be much in excess of  $\tan 2^\circ$  (0.03). Some creationists have accepted the explanation, and focused on its catastrophic nature—a high speed detachment.<sup>35,60</sup> But note serious objections to this. The physics of the gas ‘cushion’, pressures, sustainability, etc., which supposedly allowed the block to ‘float’, have not been evaluated. In particular, since heat would be needed to release the CO<sub>2</sub> from the underlying strata, abrasive friction is needed first. It is physically impossible to have the effect happen before the cause. Furthermore, if the ‘slide’ achieved the proposed velocity, perhaps 200 km/h,<sup>61</sup> what happened when the cushion was exhausted? With the surfaces now back in grinding contact, the block would have taken at least  $\sim 1,000$  m to skid to a halt, thereby leaving a 1–10 m layer of breccia along the interface.<sup>26</sup> It isn’t there.

Without a viable mechanism, there is no reason to accept the thrust explanation, leaving it a well-documented glaring exception to the geological column. Otherwise

‘Enlightenment’ motives again usurp even the simple laws of motion developed by Newton.

### Summary and recommendations

We have traced how overthrusting has been identified, and attempts made to explain the general principles within the uniformitarian paradigm over the last 200 years. It remains paradoxical, both because of the physical problems explaining the movements and inability to palaeo-reconstruct. Obviously the overthrusting paradox disappears if we are freed from the template of the geological column. Taking into account the technical issues discussed above and the subverting motives which still persist from the days of ‘The Enlightenment’, everything points firmly to the fallibility of the geological column.

Therefore we can still say that Price’s dictum: “that the whole idea of overthrusting was devised by geologists simply to salvage the dogma of fossil sequence” is true and Young’s criticism of him is wrong. If the column is not a reliable template to Earth’s strata, then an edifice of secular natural history is wrong.

Sadly, Christians and even young-earth creationists are divided about the geological column. There have been calls for all interested parties to participate more actively in forums to explore the differences as the number of challenges to the column increases rather than stay in their own corners. The prize is enormous—nothing other than a full-fronted challenge to a world that swung away from truth.

### References

1. We use ‘overthrust’ to mean any implied large-scale movement of this sort. It is a generic term encompassing ‘thrusts’, ‘nappes’, ‘slides’, ‘detachments’, and ‘shallow-angle reverse faults’. We exclude folding from this discussion because of very different mechanisms.
2. Briegel, U., Rock mechanics and the paradox of overthrusting tectonics; in: Briegel, U. and Xiao W. (Eds.), *Paradoxes in Geology*, Elsevier, Amsterdam, 2001.
3. Audley-Charles, M.G., Geometric problems and implications in large-scale overthrusting in the Banda Arc-Australian margin collision zone; in: McClay, K. and Price, N.J. (Eds.), *Thrust and Nappe Tectonics*, Special Publications 9, Geol. Soc., London, pp. 407–416, 1981.
4. Humphreys, D.R., Accelerated nuclear decay: a viable hypothesis? in: Vardiman, L., Snelling, A. and Chaffin, E. (Eds.), *Radioisotopes and the Age of the Earth*, ICR, El Cajon, CA, pp. 333–379, 2000.
5. Matthews, J.D., Was the UK once totally under water? *J. Creation* 27(1):107–113, 2013.
6. Sibley, A.M., *Cracking the Darwin Code—Exploring the Non-Scientific Foundations of Deep Time and Evolution*, Fastnet Publications, Devon, 2013.
7. Mortenson, T., The historical development of the old-earth geological timescale; in: Reed, J.K. and Oard, M.J. (Eds.), *The Geologic Column*, CRS, Chino Valley, AZ, pp. 7–30, 2006.
8. Winchester, S.B.A., *The Map that Changed the World*, Viking, London, 2001.
9. Ogg, J.G., Ogg, G. and Gradstein, F.M., *The Concise Geological Time Scale*, Cambridge University Press, Cambridge, 2008.
10. Matthews, J.D., The stratigraphic geological column—a dead end, *J. Creation* 25(1):98–103, 2011.

11. Reed, J.K., Klevberg, P. and Froede, C.R., Interpreting the rock record with the uniformitarian geologic column; in: Reed, J.K. and Oard, M.J. (Eds.), *The Geologic Column*, CRS, Chino Valley, 2006.
12. Lyell, C., *Principles of Geology*, 9<sup>th</sup> edn, D. Appleton & Co., New York, p. 54, 1854; [www.gutenberg.org/files/33224/33224-h/33224-h.htm](http://www.gutenberg.org/files/33224/33224-h/33224-h.htm), accessed 11 December 2015.
13. Lyell, K.M., *Life, Letters and Journals of Sir Charles Lyell, BART* (Original 1881), reprinted Cambridge University press, Cambridge, 2011.
14. Holmes, A., *Principles of Physical Geology*, revised by Holmes, D., Chapman and Hall, London, 1978.
15. Matthews, J.D., The origin of oil—A creationist answer, *Answers Res. J.* 1:145–168, 2008.
16. Hsu, K.J., Role of cohesive strength in mechanics of overthrust faulting and of landsliding, *Bull. Geol. Soc. Amer.* 80:927–952.
17. Price, N.J. and Cosgrove, J.W., *Analysis of Geological Structures*, Cambridge, 1990.
18. Murrell, S.A.F., The rock mechanics of thrust and nappe formation; in: McClay, K. and Price, N.J. (Eds.), *Thrust and Nappe Tectonics*, Special Publications 9, Geol. Soc., London, pp. 99–108, 1981.
19. Hubbert, M.K. and Rubey, W.W., Role of fluid pressures in mechanics of overthrust faulting, *Bull. Geol. Soc. Amer.* 70(1):115–166, 1959; p. 115.
20. Wiltchko, D.V., Thrust sheet at a ramp: summary and extensions of an earlier model; in: McClay, K. and Price, N.J. (Eds.), *Thrust and Nappe Tectonics*, Special Publications 9, Geol. Soc., London, pp. 55–63, 1981.
21. Price, N.J. and McClay, K.R., Introduction; in: McClay, K. and Price, N.J. (Eds.), *Thrust and Nappe Tectonics*, Special Publications 9, Geol. Soc., London, pp. 1–5, 1981.
22. Arkell, W.J., *The Geology of the Country around Weymouth, Swanage, Corfe and Lulworth*, Her Majesty's Stationery Office, London, 1947.
23. Ameen, M.S. and Cosgrove, J., Kinematic analysis of the Ballard Down Fault, Swanage, Dorset, *Proc. Geol. Assoc.* 101(2):119–129, 1990.
24. Ameen, M.S. and Cosgrove, J., An upper strain detachment model for the Ballard Down Fault: Discussion, *Proc. Geol. Assoc.* 101(4):303–320, 1991.
25. Carter, D.C., An upper strain detachment model for the Ballard Down fault: Discussion, *Proc. Geol. Assoc.* 102:309–320, 1991.
26. Scholz, C.H., Wear and gouge formation in brittle faulting, *Geol. Soc. Amer.* 15:493–495 1987.
27. Price, G.M., *Evolutionary Geology and the New Catastrophism*, Pacific Press, Mountain View, CA, 1926.
28. Young, D.A., *The Biblical Flood—A Case Study of the Church's Response to Extrabiblical Evidence*, Paternoster Press, Carlisle, UK, 1995.
29. Morris, H.M., *History of Modern Creationism*, Master Books, Green Forest, AR, 1984.
30. Nelson, B., *The Deluge Story in Stone*, Bethany Fellowship, Minneapolis, MN, 1968.
31. Whitcomb, J.C. and Morris, H., *The Genesis Flood*, Presbyterian and Reformed Publishing, Phillipsburgh, NJ, 1961.
32. Scott, R.A., Smyth, H.R., Morton, A.C. and Richardson, N. (Eds.), *Sediment Provenance Studies in Hydrocarbon Exploration and Production*, Special Publications 386, Geol. Soc., London, 2014.
33. Jaeger, J.C., Cook, N.G.W., and Zimmerman, R.W., *Fundamentals of Rock Mechanics*, 4<sup>th</sup> edn, Blackwell, Oxford, 2007.
34. Lammerts, W.E., Recorded instances of wrong-order formations: part viii, *Creation Res. Soc. Quart.* 24(1):46–47, 1987.
35. Garner, P., *The Genesis Flood 50 years on, Origins (BCS)* 55:4–10, 2011.
36. Snelling, A.A., *Earth's Catastrophic Past*, Institute for Creation Research, Dallas, TX, 2009.
37. Tyler, D., Accept the column, reject the chronology; in: Reed, J.K. and Oard, M.J. (Eds.), *The Geologic Column*, CRS, Chino Valley, AZ, pp. 53–71, 2006.
38. Alexander, D., *Rebuilding the Matrix*, Lion Hudson, Oxford, 2001.
39. Alexander, D., *Creation or Evolution—Do We Have To Choose?* Monarch Books, Oxford, 2008.
40. Nield, T., Fighting the good fight, *Geoscience* 18(1):3, 2008.
41. Gould, S.J., *Wonderful Life—The Burgess Shale*, Norton, New York, 1989.
42. Walker, T., The Geological Society of London uses bully tactics, [www.creation.com/the-geological-society-of-london-uses-bully-tactics](http://www.creation.com/the-geological-society-of-london-uses-bully-tactics), 13 May 2008.
43. Alexander, D. and White, R.S., *Beyond Belief: Science, Faith and Ethical Challenges*, Lion Hudson, Oxford, 2004.
44. Berry, R.J., *Christians and Evolution*, Monarch, Oxford, 2014.
45. Matthews, J.D., Creationism, evangelism and that bothersome debate? A review of *Christians and Evolution* by R.J. Berry, *J. Creation* 29(3):28–32, 2015.
46. Conway Morris, S., *The Crucible of Creation*, Oxford, 1998.
47. Forster, P. and Marston, R., *Reason, Science and Faith*, Monarch Books, Crowborough, UK, 1999. Reviewed by Kulikovsky, A., *J. Creation* 16(2): 31–36, 2002.
48. Johnson, R.J., *Genesis, Geology and Catastrophism*, Paternoster Press, Exeter, UK, 1988.
49. Lucas, E., *Genesis Today—Genesis and the Questions of Science*, Scripture Union, London, 1989.
50. Polkinghorne, J., *Science and Creation*, SPCK, London, 1988.
51. Wright, R.T., *Biology through the Eyes of Faith*, Apollos, Leicester, 1991.
52. Holm, G.M., Distribution and origin of overpressure in the Central Graben of the North Sea; in: Law B.E., Ulmishek, G.F. and Slavin, V.I. (Eds.), *Abnormal Pressures in Hydrocarbon Environments*, AAPG Memoir 70:123–144, 1998.
53. Evans, D.C., Graham, C., Armour, A. and Bathurst, P., *The Millennium Atlas: Petroleum Geology of the Central and Northern North Sea*, London, The Geological Society, 2003.
54. Muggeridge, A., Abaioglu, Y., England, W. and Smalley, C., The rate of pressure dissipation from abnormally pressured compartments, *Bull. Amer. Assoc. Petro. Geol.* 89(1):61–80, 2005.
55. Murchison, R.I., On the geological structure of the Alps, *Quart. J. Geol. Soc. V(I) Dec.* 13:157–313, 1848.
56. McClay, K.R. and Coward, M.P., The Moine Thrust Zone: an overview; in: Price, N.J. and McClay, K.R. (Eds.), *Mechanics of Thrust Nappes*, London, Special Publications, Geological Society, pp. 241–260, 1981.
57. Johnstone, G.S. and Mykura, W., *The Northern Highlands of Scotland*, Her Majesty's Stationery Office, London, 1989.
58. Trewin, N.H. (Ed.), *The Geology of Scotland*, The Geological Society, London, 2002.
59. Butler, R.W.H., The nature of 'roof thrusts' in the Moine Thrust belt, NW Scotland: its implications for the structural evolution of thrust belts, *J. Geol. Soc.* 161(5):849–860, 2004.
60. Oard, M., The Heart Mountain catastrophic slide, *J. Creation* 20(3):3, 2006.
61. Craddock, J.P., Geary, J. and Malone, D.H., Vertical injectites of detachment carbonate ultracataclasite at White Mountain, Heart Mountain detachment, Wyoming, *Geology* 40:463–466, 2012.

**Dr John D. Matthews** is a retired chartered geologist (EurGeol) from the oil industry. He holds a B.Sc. in Mathematics (1958–1961) and a Ph.D. in Earth Science (2000–2004) completed in a university department specializing in petroleum engineering and rock mechanics.



# DNA topoisomerases—the ‘relaxers’ and ‘unknotters’ of the genome

Joe Deweese

Living organisms must access, maintain, and duplicate the genetic information found in DNA. To utilize or copy the information in DNA, the strands of the double helix must be able to separate, but this process causes excessive twisting of the double helix known as supercoiling. Supercoiling must be carefully monitored and maintained for DNA metabolism to take place. Cells employ a family of enzymes known as DNA topoisomerases to maintain the topological state of DNA and to allow routine cellular processes like transcription and replication to occur. Topoisomerases reversibly cut one or both strands of the double helix in order to resolve supercoiling, knotting, and tangling in the DNA. Without topoisomerases, transcription and replication could not occur because of excessive positive supercoiling associated with separating the strands of DNA. Topoisomerases are also responsible for unlinking sister chromatids following replication so that the chromosomes can be segregated properly during mitosis. Further, topoisomerases do not conform to standard evolutionary phylogenies and require multiple independent origins (described as ‘convergent evolution’) to explain the various classes. Topoisomerases represent a fascinating family of enzymes that play a critical role in cellular life.

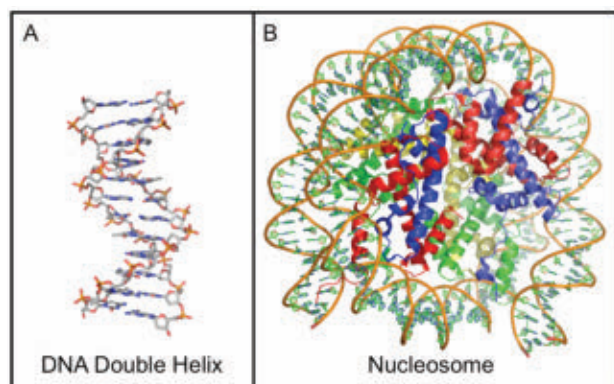
**B**iological life as we know it is dependent on instructions, most of which come in the form of genetic information contained in DNA. The human genome exists as 46 segments of DNA called chromosomes, which in most of our cells consists of 2 copies of chromosomes 1–22 plus either XX or XY. Human chromosomes vary in length and consist of around 100 to 200 million base pairs (bp, pairs of nucleotides, which are the monomers of nucleic acids) each and together add up to around 6 billion bp. If these chromosomes were stretched out from their compacted form and lined up, there would be around 2 m of DNA per human cell! This set of chromosomes is found in every body cell except those lacking a nucleus (e.g. mature red blood cells) or the reproductive cells, which contain one copy of each chromosome rather than two.

While the information encoded by the nucleotide bases exists as a linear sequence, it is compacted in the form of the double helix we know as the structure of DNA (figure 1A). The double helix is an elegant form with very precise structural constraints. From a cellular perspective, the picture is more complex, as the double helix exists in a nuclear matrix and is compacted by winding around histone proteins (in eukaryotes and some archaea) (figure 1B). The typical image of a chromosome ‘spread’ or karyotype shows the fully compacted forms of the chromosomes as they exist during cell division, which represent a compaction of around 10,000 fold. During other parts of the cell cycle, chromosomes exist in dynamic states of compaction depending on which regions of the genome are needed in a given cell type.

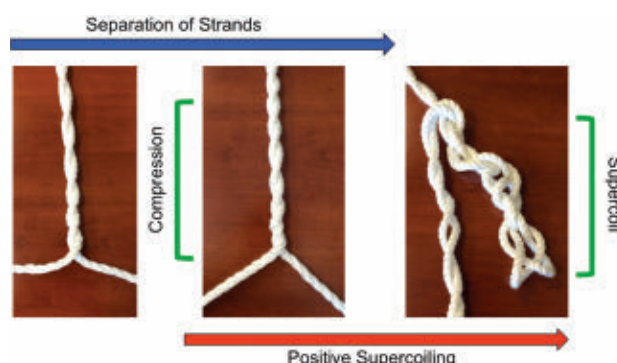
This leads us to some interesting questions: how does the cell access compacted regions of the genome for transcription and replication? What challenges are faced when dealing with the double helical nature of the DNA? Further, how does a cell deal with the enormous amount of genetic information in the nucleus? James Watson and Francis Crick understood that the double helix itself would pose certain challenges to the cell. However, their confidence in their structure left them to conclude: “we feel that these objections will not be insuperable.”<sup>1</sup> Their understanding of nuclear processes was far less developed than our modern understanding, but their foresight proved to be accurate.

To envision the problem, imagine a double-stranded rope where the strands are wrapped around each other into a double helix (figure 2). Trying to separate these ropes by simply pulling the two strands apart is quickly met with resistance because they are wound around one another (assuming the duplex is extremely long or the opposite end is fixed in space and cannot untwist freely). As seen in figure 2, strand separation leads to the ropes becoming more tightly wound ahead of the separation. Overwinding causes supercoiling, which looks similar to an old-fashioned telephone cord that has become twisted (see figure 2). If there is no way to relieve this torsional strain, the separation of strands will be halted. The same challenges exist for our DNA when the strands of the double helix are separated.<sup>2</sup>

For example, during replication DNA helicases ‘unzip’ the strands of DNA in an ATP-dependent process in order for DNA polymerases to copy the DNA. However, the work of the helicases results in torsional strain and supercoiling within the DNA strands that must be relieved for replication



**Figure 1.** Panel A: Stick diagram of DNA double helix segment. Structure from PDB ID 1BNA. Panel B: Ribbon and line diagram of crystal structure of DNA wrapped around histone proteins to form a nucleosome. Structure from PDB ID 5AV5. Images generated using Pymol.



**Figure 2.** Supercoiling results from pulling apart coiled strands. As the ends of a double-stranded coil are pulled apart, the coils become compressed. If the compression is not relieved, it will result in supercoils. These are termed positive supercoils.

to continue.<sup>2</sup> Furthermore, transcription involves strand separation mediated by the RNA polymerase and faces positive supercoiling as seen with replication.<sup>2</sup> These are critical challenges in the cell. If separating the DNA strands for replication and transcription is necessary yet causes torsional strain, how could cells survive unless there was a mechanism to alleviate this problem?

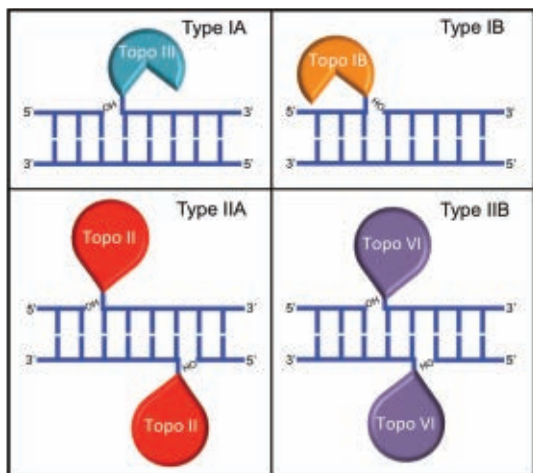
As it turns out, Watson and Crick were right—the challenges were not ‘insuperable’! In fact, cells overcome these challenges by using a family of enzymes known as DNA topoisomerases. A topoisomerase is an enzyme that identifies the topology (topo-) of DNA and alters the three-dimensional conformation of it (-isomerase), without changing the chemical nature. The end result is that topoisomerases relieve strain and also remove knots and tangles.

### Types of topoisomerases

Topoisomerases are classified based on the structures and mechanisms of the specific classes. There are two primary types: I and II. Within these types are several subclasses (i.e. IA, IB, IC) that differ in specific details (table 1).<sup>2–4</sup> Broadly speaking, type I enzymes cut one strand of the DNA double helix while type II enzymes cut both strands of the DNA (figure 3).<sup>4</sup> In both type I and II enzymes, this involves an active site tyrosine amino acid becoming covalently bonded to either the 3’ or 5’ end of the cleaved DNA. Conveniently, type I topoisomerases have been named with odd numbers (I, III, V) while type II topoisomerases have been named using even numbers (II, IV, VI, VIII).<sup>3,4</sup>

**Table 1.** Families of topoisomerases and representative examples. Domains where specific enzymes are found is denoted: A, archaea; B, bacteria; E, eukaryote. Activity is classified by the ability to support relaxation (rel) or supercoiling (sup) and the direction of supercoiling is denoted: – for negative supercoils and + for positive supercoils. Representative species are denoted at right. It should also be noted that there are viral topoisomerases in the IA, IB, and IIA families that are not shown in the table above.

Family	Enzyme	Linkage	Mechanism	Cofactors	Activity	Rep. Species
IA	topoisomerase I (B) topoisomerase III(a,b) (E) topoisomerase III (A, B) reverse gyrase (A)	5'	enzyme-bridged strand passage	Mg <sup>2+</sup>	rel -	<i>E. coli</i> <i>H. sapiens</i>
				Mg <sup>2+</sup> , ATP	sup +	<i>E. coli</i> <i>Sulf. acidocaldarius</i>
IB	topoisomerase IB (E, B) topoisomerase IB mitochondrial (E)	3'	controlled rotation/swiveling	none	rel -+	<i>H. sapiens</i>
IC	topoisomerase V	3'	controlled rotation/swiveling	none	rel -+	<i>M. kandleri</i>
IIA	topoisomerase II (E) topoisomerase II(a,b) (E) topoisomerase IV (B) gyrase (A,B)	5'	double-strand passage 4-bp overhang	Mg <sup>2+</sup> , ATP	rel -+	<i>S. cerevisiae</i> <i>H. sapiens</i>
					sup -	<i>E. coli</i> <i>E. coli</i>
IIB	topoisomerase VI (A, E)	5'	double-strand passage 2-bp overhang	Mg <sup>2+</sup> , ATP	rel -+	<i>Sulf. shibatae</i>



**Figure 3.** Various DNA cleavage mechanisms of topoisomerases. Topoisomerases cleave one or both strands of DNA by making a covalent link between a tyrosine on the enzyme and a phosphate of the DNA backbone. Type I topoisomerases cleave one strand of the duplex by linking to either the 5' end (type IA) or 3' end (type IB). Type II topoisomerases cleave both strands of the double helix with either a four base-pair (type IIA) or two base-pair (type IIB) stagger. It should be noted that bacterial topoisomerase I is a type IA, while mammalian topoisomerase IB is a type IB.

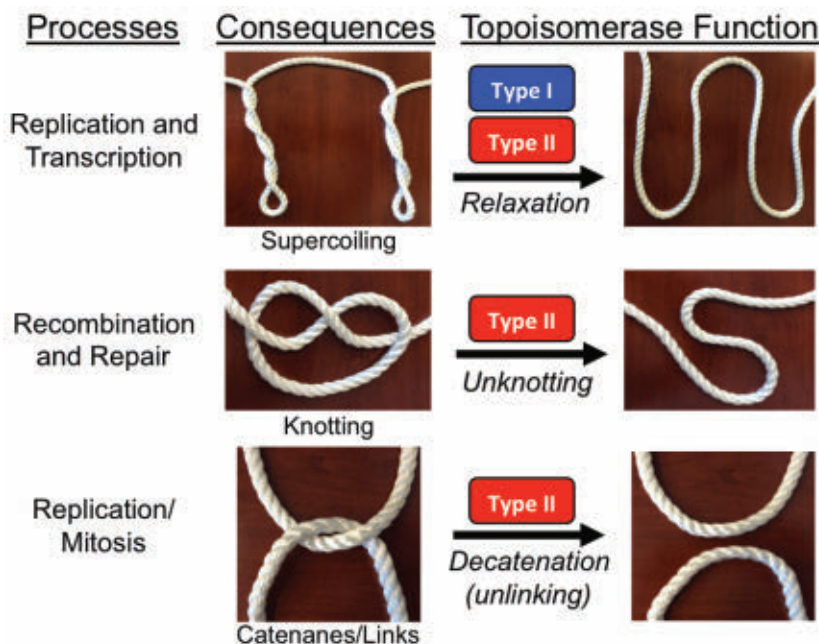
Topoisomerase function can also be described mathematically using the topology concept of linking number, which is discussed elsewhere.<sup>2</sup>

First, type I topoisomerases are generally monomeric enzymes (a single protein) that are able to: 1) bind to DNA, 2) cut one strand by forming a transient covalent bond with it, 3) relieve the torsional strain by either controlled rotation (IB/IC) or strand passing (IA), and 4) ligate (covalently reconnect) the cut DNA strand back together and release the DNA (figure 3).<sup>4</sup> The process facilitated by most type I topoisomerases is known as relaxation because it 'relaxes' supercoils in the DNA (figure 4). This is needed during both DNA replication and transcription of RNA. There are other roles for specific subclasses of type I topoisomerases, including the resolution of recombination intermediates.<sup>3</sup>

Type I topoisomerases are present in all known life forms and are referred to by several specific names. For example, bacterial topoisomerase I, known as the  $\omega$  protein (lower-case

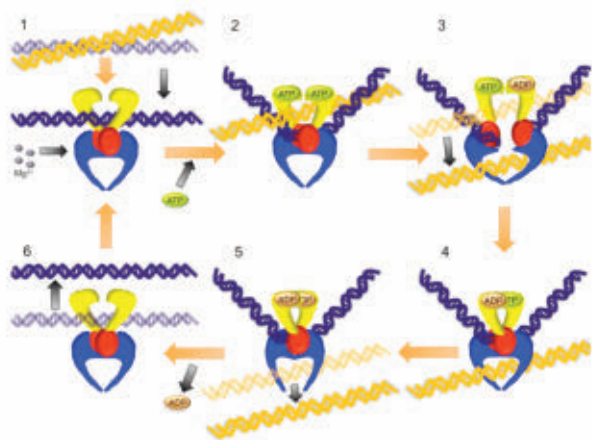
omega), is the first topoisomerase ever discovered.<sup>5</sup> Jim Wang of Harvard University discovered the  $\omega$  protein while searching for factors that seemed to change the supercoiling of bacterial DNA, which turned out to be a type IA topoisomerase in bacteria.<sup>5,6</sup> Humans have two type IA topoisomerases known as topoisomerase III $\alpha$  and III $\beta$ , which are present in the nucleus.<sup>3</sup> Interestingly, there are also two type IB enzymes in humans known as topoisomerase IB and mitochondrial topoisomerase IB (Top1mt).<sup>7,8</sup> These enzymes primarily differ in the N-terminal domain, where the nuclear form has a nuclear localization sequence and Top1mt has a mitochondrial targeting sequence (and lacks about 150 amino acids found in the nuclear form N-terminus).<sup>9</sup>

Second, the type II topoisomerases involve a related but more complex mechanism.<sup>2,10,11</sup> These enzymes are generally homodimers or heterotetramers (A<sub>2</sub>B<sub>2</sub>), utilize ATP, and often require a metal cofactor (Mg<sup>2+</sup>).<sup>2,10,11</sup> Type II topoisomerases 'recognize' helix-helix crossovers (see catenanes/links depicted in figure 4). As seen in figure 5, the enzyme works by: 1) binding at a crossover, 2) cleaving both strands of one double helix (the Gate- or G-segment), forming a covalent bond with the 5' ends, 3) separating the ends of the broken segment of DNA (DNA gate) and passing the intact double helix, known as the



**Figure 4.** Topological consequences of biological processes and the alleviation of these challenges by topoisomerases. The figure above depicts a summary of some of the topological challenges addressed by topoisomerases. Note that in this figure, a single strand of the rope represents the double helix. Replication and transcription both cause positive supercoiling of the DNA, and this can be alleviated by type I and type II topoisomerases in a process called relaxation. Recombination and DNA repair may involve knots that can be removed by type II topoisomerases. Replication results in chromosomes that are catenated or linked. Type II topoisomerases can relieve these links so that mitosis can occur and chromosomes can segregate.





**Figure 5.** Catalytic cycle of type IIA topoisomerases. Topoisomerase II is depicted with distinct domains in different shading (top, grey: N-terminal ATPase domain; light grey: central TOPRIM domain; and dark grey: C-terminal domain). Some details are omitted for clarity. 1) The enzyme binds to a helix-helix crossover (DNA in light and dark grey). DNA cleavage is dependent upon metal ions (spheres). 2) The gate segment (G-segment) of DNA in dark grey is bent and cleaved. The transport segment (T-segment, light grey) is captured by the N-terminal clamp in the presence of ATP. 3) The G-segment is opened and hydrolysis of one molecule of ATP to ADP induces strand passage of the T-segment. 4) After strand passage, the G-segment closes. 5) The C-terminal gate is opened to release the T-segment. ATP is also hydrolyzed to ADP in this step. 6) The enzyme releases the G-segment and is set for another round of catalysis.

Transport- or T-segment, through the break in an ATP-dependent manner, 4) closing the ‘DNA gate’ and ligating the G-segment, 5) releasing the T-segment, and 6) releasing the G-segment. The enzyme then is set to catalyze the reaction again as needed.

Bacteria generally have two type II topoisomerases: DNA gyrase and topoisomerase IV. Gyrase works in a distinct manner from that of many other topoisomerases since these enzymes negatively supercoil DNA while other type II enzymes can only convert a molecule from supercoiled to relaxed. We will not go in to the mechanism in detail here, but reviews are available in the literature.<sup>12</sup>

In mammals, we find two versions of the type II enzyme: topoisomerase II $\alpha$  and topoisomerase II $\beta$ .<sup>10</sup> From a broad perspective, there are many similarities in these enzymes so they are often generically referred to as topoisomerase II or Top2. However,

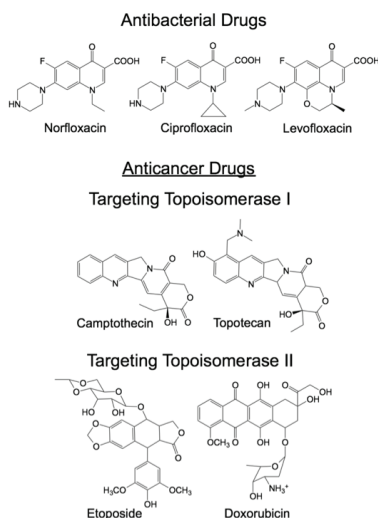
they differ in size (by around 100 amino acids), are expressed from distinct genes on separate chromosomes, and only share around 70% amino acid identity.<sup>10</sup> Further, there are some functional differences. For example, topoisomerase II $\alpha$  is generally considered to be active during replication and mitosis while topoisomerase II $\beta$  is active during transcription.<sup>13–16</sup> Topoisomerase II $\alpha$  expression levels rise and fall during the cell cycle while topoisomerase II $\beta$  remains more constant.<sup>13,17–21</sup> Topoisomerase II $\beta$  is considered a housekeeping gene since all nucleated cells express it to support transcription.<sup>22–24</sup> Interestingly, the main difference between the sequences of  $\alpha$  and  $\beta$  is in the C-terminal domain (less than 35% identity). This region is responsible for the differences in functional capabilities and influences the selection of substrate.<sup>15,25</sup>

### Cellular roles and essential functions

What roles do these enzymes play in cells? In order to understand the functions, it is important to consider how the topology of DNA is altered by routine cellular processes. In biological systems, DNA exists in a supercoiled state.<sup>2</sup> As noted earlier, supercoiling is essentially what happens to a coiled telephone cord that becomes excessively twisted over time (see figure 2). Coiled cords tend to become supercoiled until at some point they are unwound (usually out of frustration!). DNA generally exists in a state that

is slightly negatively supercoiled, which means that the double helix is slightly opened compared to a fully relaxed DNA segment.<sup>2</sup> During the processes of transcription and replication, DNA strands are separated and become positively supercoiled to compensate for the strand separation. If left unresolved, excessive supercoiling will inhibit replication and transcription. Both type I and type II topoisomerases are able to relieve supercoiling that results from these processes by working ahead of replication forks and transcription bubbles (figure 4).<sup>26</sup> It has been found that type I enzymes are essential in a number of different organisms, probably because of the role of type I topoisomerases in relaxation, though other roles also exist.<sup>8</sup>

Additionally, the type II enzymes are also involved in unknotting and unlinking DNA molecules (figure 4).<sup>10</sup> Replication is the process by which



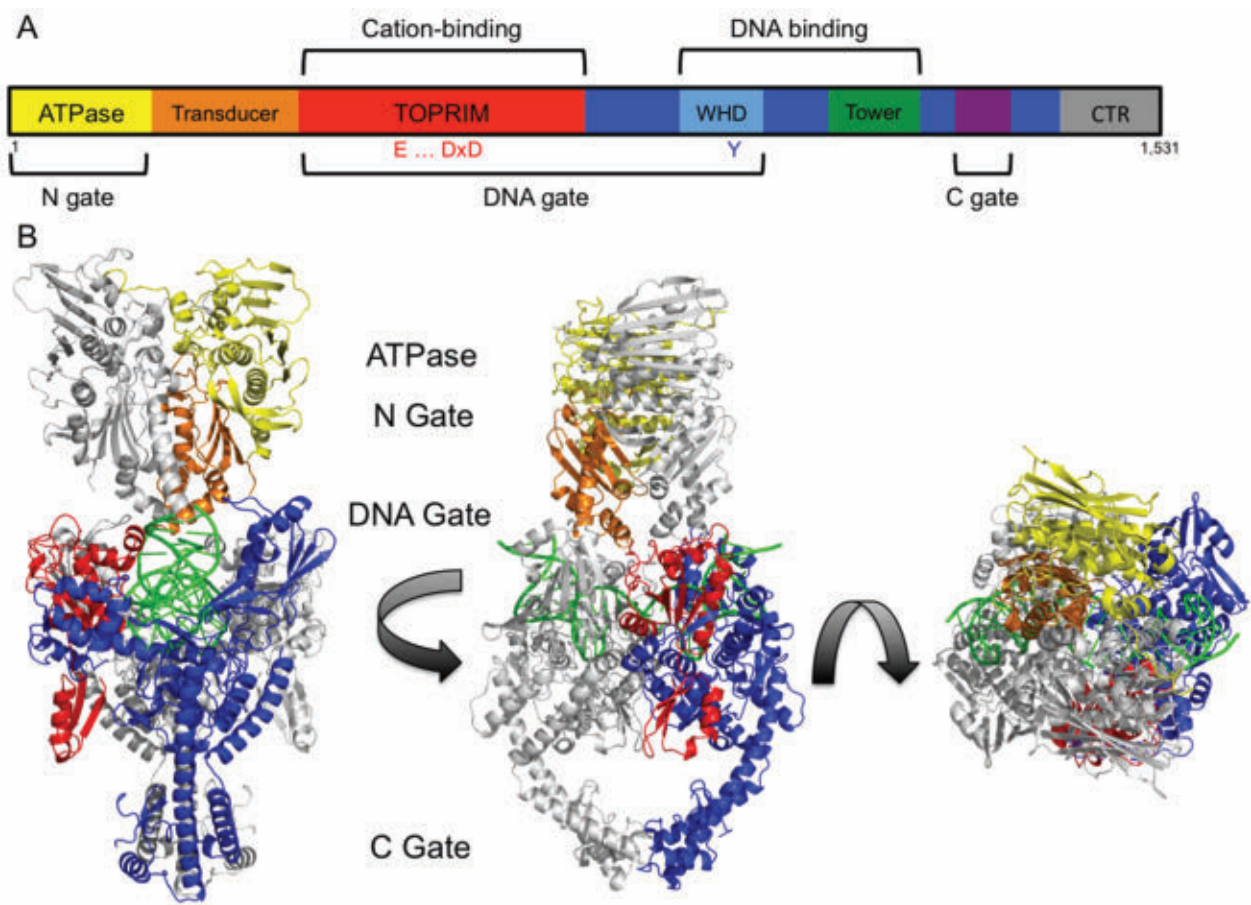
**Figure 6.** Topoisomerases are targeted for therapeutic purposes. Bacterial topoisomerases are targeted by agents such as norfloxacin, ciprofloxacin, and levofloxacin. Human topoisomerases can be targeted by anticancer agents targeting topoisomerase I (camptothecin and topotecan) or topoisomerase II (etoposide and doxorubicin).

chromosomes are copied and results in the sister chromatids (the products of replication of a single chromosome) being wound around each other or catenated.<sup>2,10</sup> Decatenation is the technical term used to describe the process of separating linked chromosomes (figure 4). Only type II topoisomerases can decatenate and this is considered to be the essential function of type II topoisomerases.<sup>2,4,10</sup> Evidence suggests that the progress of decatenation can serve as a cell cycle checkpoint during mitosis and promotes genomic stability by ensuring the proper separation of sister chromatids.<sup>27</sup> Thus, all known living organisms have at least one isoform of the type II enzyme.<sup>3,8</sup> Further, topoisomerase II $\alpha$  is essential in mammalian cells as it serves the role of decatenating linked chromosomes.<sup>10</sup> Cellular DNA in eukaryotes and some other life forms exists as a complex of protein and DNA known as chromatin. Chromatin is condensed and decondensed depending on epigenetic regulation and the phase of the

cell cycle, which again relies on type II topoisomerases.<sup>10</sup> Aside from these roles, there is a topoisomerase-like protein known as Spo11, which is involved in creating strand breaks associated with meiosis, but this is beyond the scope of the current discussion.<sup>28–30</sup>

### Therapeutic targeting

As a result of the universal nature of these enzymes and their essential functions in living organisms, they are also used as therapeutic targets (figure 6).<sup>31</sup> In particular, bacterial versions are targeted by antibacterials like levofloxacin (targeting a bacterial topoisomerase II).<sup>31</sup> In addition, mammalian topoisomerases can be targeted by a number of anticancer drugs such as camptothecin and topotecan, which target topoisomerase I, and doxorubicin and etoposide, which target topoisomerase II.<sup>11,31</sup> These agents generally



**Figure 7.** Domain structure diagram and crystal structure images of a type IIA topoisomerase. A) The general domain structure of a type IIA topoisomerase. Size and spacing of segments is approximate. Amino acid numbers correspond to human topoisomerase II $\alpha$ . Location of acidic amino acids in the TOPRIM (E, D) and the active site tyrosine (Y) are denoted. The variable C-terminal region is also depicted (CTR). B) Ribbon diagram images generated from a crystal structure of *Saccharomyces cerevisiae* topoisomerase II (PDB ID 4GFH; residues 1–1177). Images show a 'side', 'front', and 'top' view, respectively. One protomer is shown in all grey. The other protomer is in shades of grey with approximate locations of key domain segments denoted. It should be noted that this structure does not include the C-terminal region. Images generated using Pymol.



work by preventing the enzyme from completing the catalytic cycle, which causes an accumulation of single- and double-stranded DNA breaks.<sup>11,31</sup> Therefore, they are often called topoisomerase poisons.<sup>11,31</sup>

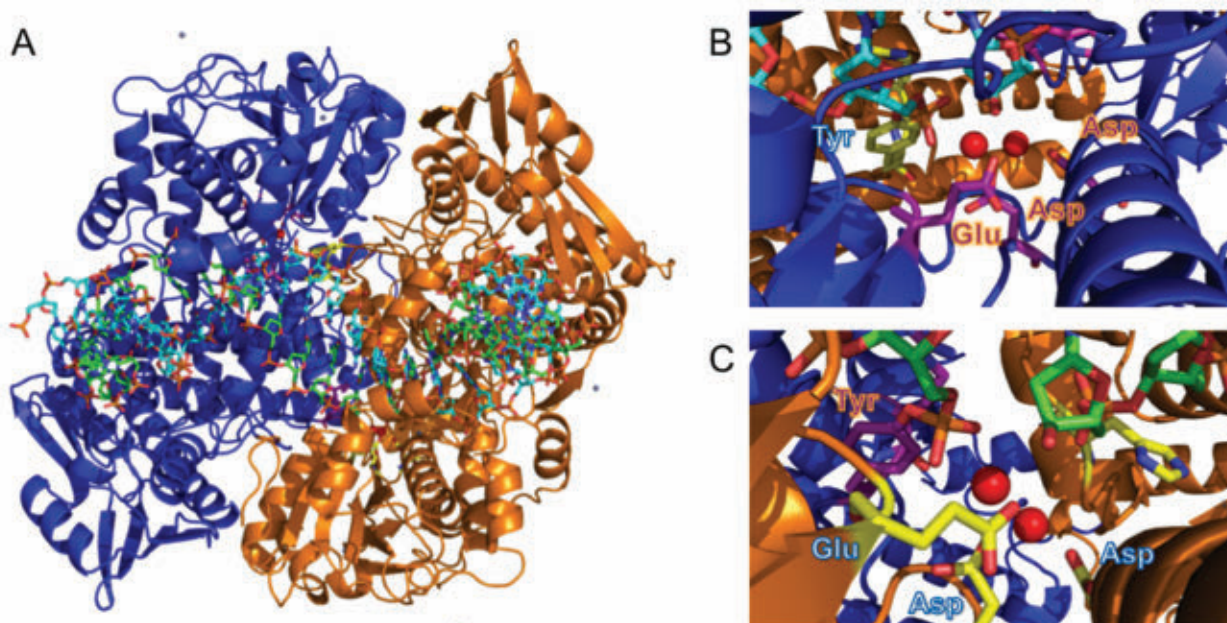
In contrast, a separate class of compounds, known as catalytic inhibitors, interrupt enzyme function by preventing ATP hydrolysis.<sup>31</sup> What is unique about these compounds is that cell death is not promoted by overwhelming the cell with DNA damage. These compounds block catalytic activity, which prevents topoisomerase II from participating in transcription- and replication-associated topology regulation.<sup>2,32</sup> Consequently, cells will get ‘stuck’ and will be unable to complete cell division. While theoretically this class of compounds should be useful for specific purposes, there are only a few examples of clinically relevant catalytic inhibitors.<sup>31</sup> Ongoing research is continuing to explore new options for this pathway.<sup>33</sup>

### Type IIA topoisomerases—a more detailed look

Let us focus on the second class of enzymes and examine in more detail the intricate design of this molecular machine. Specifically, we will examine the eukaryotic topoisomerase II enzymes, which are homodimeric (two copies of the same protein), multi-domain proteins.<sup>10,31</sup> Each protomer is ~1500–1600 amino acids depending on the specific isoform,

which makes this a rather large dimer (over 300 kDa). The general primary sequence includes: 1) an N-terminal ATPase domain; 2) a centrally located cleavage-and-ligation domain, and 3) a C-terminal variable domain (figure 7). This simplification leaves out the fact that several key features in this protein only exist in the three-dimensional structure.

First, topoisomerase II is a homodimeric enzyme with twofold axis of symmetry (figure 7). An amazing feature of the symmetrical nature of the enzyme is that the protein makes multiple points of contact between the protomers that are able to be alternately separated and rejoined. The full structure has three ‘gates’: an N-terminal upper gate, a C-terminal lower gate, and a centrally-located ‘DNA gate’. Further, the separation of these gates is coordinated such that two points of contact are maintained during catalysis (figure 5).<sup>34</sup> For example, if the N-terminal gate is open, the DNA gate and lower gate are closed. To open the DNA gate, the N-terminal gate closes. Once the strand passage is completed, the DNA gate closes and allows the C-terminal gate to open. This coordination is amazing considering the machine involved is a protein made of amino acids. This type of coordination requires the enzyme to be able to cycle through various states of opening/closing in a concerted manner. These conformational changes in the protein are regulated by various factors including the presence of DNA,



**Figure 8:** A crystal structure of a covalent topoisomerase II:DNA complex shows cooperation between the two protomers. A crystalized core of truncated yeast topoisomerase II (missing portions of the N- and C-terminus) is shown in complex with a segment of DNA. A) Top view showing protomers in light and dark grey with DNA through the central cavity. B and C) A close-up view of the two active sites. Critical residues from each half cooperate in cleavage and ligation including the active site tyrosine (Tyr) and glutamic (Glu) and aspartic acid (Asp). Residues from the light grey protomer are highlighted in light font while those from the dark grey protomer are highlighted in dark font. The spheres represent two metal ions. The active site tyrosine is covalently linked with the 5' end of the cleaved DNA. Images were generated from PDB ID 3L4K using Pymol.



the topology of DNA, and the availability of ATP and metal ion cofactors.

Second, the axis of symmetry also sets up a very interesting scenario. For topoisomerase II to cleave DNA, there is a specific arrangement of amino acids in the active site (figure 8). This includes the TOPRIM (topoisomerase-primase) domain where several acidic amino acids form a characteristic motif (E ... DxD) that coordinates  $Mg^{2+}$  ions.<sup>35</sup> Also, there are other amino acids that appear to play a role in the process such as an arginine and a histidine.<sup>36</sup> Further, the active site amino acid is tyrosine. Tyrosine has a hydroxyl (–OH) that is able to attack the backbone of DNA at a phosphate group in concert with the adjacent  $Mg^{2+}$  ions coordinated by the TOPRIM domain. The phosphate backbone is broken and the 5'-phosphate group is bound to the tyrosine. This leaves a free 3'-OH group on the other side of the break. Intriguingly, both active sites require amino acids from each half of the protein. The metal-ion coordinating residues of the TOPRIM domain come from one protomer and the active site residue and some others come from the other protomer.<sup>36</sup> So, the active site only exists as a whole when the DNA gate is closed (figure 8). Once the cleavage/ligation domain separates (opening the DNA gate), the active site residues are no longer in proximity, which maintains the DNA/enzyme linkage. Amazingly, the metal-ion-binding amino acids are in the correct place within the primary sequence so that in the folded, quaternary structure they are appropriately located adjacent to the opposing protomer's active site tyrosine prior to opening of the DNA gate (figure 8).

This design feature ensures that the DNA is brought back together, allowing the ends to line up, before the enzyme catalyzes the ligation reaction and releases the DNA.<sup>37,38</sup> Further, the mechanism is balanced in a way that the enzyme preferentially ligates rather than cleaves—keeping these enzymes from simply ‘chewing up’ the genome.<sup>39</sup> The transient nature of the interaction helps avoid situations where enzyme-DNA complexes exist as ‘road blocks’ to the transcription or replication machinery. It is precisely this interaction that is hijacked by several of the therapeutic agents mentioned above. The stabilization of this complex on DNA leads to DNA strand breaks and DNA damage.<sup>11</sup>

Third, the enzyme contains a DNA binding groove, complete with positive charges, attracting the DNA backbone that is negative at normal cellular pH, and two ‘clamps’ large enough to accommodate a double helix. Together, this demonstrates that topoisomerase II is well-suited to handle and manipulate DNA. The DNA binding groove again involves proper alignment of the axis of symmetry of the protomers to allow for the G-segment to bind in the active site for cleavage. Further, the upper and lower clamps accommodate the transport segment before and after strand

passage, respectively. According to structural evidence, the active site tyrosine actually shifts after DNA cleavage, which moves ‘levers’ in the enzyme and closes the C-gate.<sup>36</sup> Again, the key arrangement of nucleotides in three-dimensional space is critical for this structure to be able to bind and manipulate DNA. Further, the enzyme actually induces an extreme bend in the G-segment supported by specific amino acids in the binding groove.<sup>36,40</sup> DNA cleavage occurs in a stepwise manner with the first strand break allowing for the second strand break to occur more rapidly.<sup>39,41</sup>

Fourth, the utilization of ATP has been an enigma for some forms of topoisomerases. The relaxation and decatenation reactions catalyzed by many topoisomerases are considered to be thermodynamically favourable. Since ATP is not needed to ‘power’ strand passage, why then is ATP required? The answer appears to be that the ATP helps maintain the contact between the two halves of the N-gate during strand passage and release in order to prevent dimer dissociation.<sup>34,42</sup> Structural evidence indicates that the ATPase domains twist or wrap around each other in the presence of ATP (figures 5 and 7).<sup>42</sup> In other words, the ATP appears to keep the dimer from falling apart while performing a unidirectional strand passage! Interestingly, evidence suggests that the ATP is hydrolyzed sequentially during the latter portion of the catalytic cycle (strand passage/ligation/strand release).<sup>43</sup> Although, the exact significance of the sequential hydrolysis is unknown. The ATPase sequence is followed by the transducer domain (figure 7). This domain is involved in ‘communicating’ to the cleavage/ligation domain when ATP is bound and likely helps coordinate the conformational changes occurring during catalysis.<sup>10,44</sup>

### Implications of topoisomerases

First, DNA topoisomerases are clearly valuable and important enzymes for life since all identified living organisms depend on DNA. Since regulation of DNA topology is fundamental and essential to life, it is not a stretch to argue that topoisomerases are required to support life as we know it. In fact, DNA topoisomerases are present in living organisms from the ‘simplest’ to the most complex and even in some viral genomes.<sup>3,8,45</sup>

This brings up an interesting quandary. Topoisomerases are encoded on the DNA that is their substrate, which raises the question of which came first: DNA or the topoisomerases responsible for alleviating torsional strain in DNA? Without topoisomerases, cells lose the ability to regulate DNA topology, which quickly halts replication and transcription. Without DNA, there would be no means for encoding the information needed to build the enzyme.

Whatever evolutionary process may be posited, it is important to point out that DNA topoisomerases would have to be present very early, as even the simplest DNA genome would have a need for the regulation of DNA topology (assuming that this genome needs somewhere close to the number of genes required for living organisms today). The same could be argued for DNA polymerases, helicases, and a host of other enzymes that function on DNA. The essential function of a number of common enzymes must be in place for this system to work. The biochemical network that ‘runs’ cells is extraordinarily interdependent—proteins, DNA, RNA, carbohydrates, lipids—all of these biomolecules rely on one another at some level! In addition, this is not a matter of natural selection driving the process since natural selection really describes differential reproduction, which requires at least two self-reproducing entities. Topoisomerases are essential for this reproduction in DNA-based organisms. Thus, differential reproduction may help us understand some of the diversity of topoisomerases, but it cannot explain the *origin* of the topoisomerases.

Second, as described earlier, DNA replication results in sister chromatid pairs that are interlinked or catenated. This problem is alleviated by type II topoisomerases, though evidence shows that not all isoforms of the type II enzymes can fulfil this function. Decatenation by type II topoisomerases must occur in order for cells to segregate chromosomes into separate daughter cells. In other words, cell division would be impossible without the decatenation activity of type II topoisomerases.<sup>10</sup> In mammals, this involves topoisomerase II $\alpha$  and not topoisomerase II $\beta$ .<sup>15</sup> For this reason, loss of topoisomerase II $\alpha$  cannot be compensated for by topoisomerase II $\beta$ .<sup>10</sup> Further, whether chromosomes are circular or linear, the problem remains because any linear chromosomes large enough to encode the complement of genes required for the simplest living organisms (e.g. 580 kbp in *Mycoplasma genitalium*<sup>46</sup>) would be too large to decatenate on their own. Decatenation by a type II topoisomerase would be needed even for genomes much smaller than 500 kbp and is required to separate even small circles of DNA (plasmids).

Third, the simplest known type II topoisomerases contain approximately 800 amino acids split between two segments. Each half of the eukaryotic enzyme is actually a separate protein in bacterial versions. Thus, the quaternary protein structure in bacterial topoisomerase II is an A<sub>2</sub>B<sub>2</sub> tetramer, which means there are two copies of the ‘A’ subunit and two copies of the ‘B’ subunit. From an evolutionary perspective, the genes for these subunits must fuse and expand over time to become what is found in eukaryotic cells (unless the eukaryotic enzymes had a distinct origin). An alternative explanation suggests that one gene (gene A, for example) gradually added features until reaching the point of no longer

needing the other gene (gene B, in this case). These scenarios would rely on natural selection along with random mutation in order to explain the consolidation of functions that were already operating in an apparently effective manner since bacterial type II topoisomerases are tetrameric (with the exception of topoisomerase VIII, a recently discovered topoisomerase that is dimeric and distinct from type IIA and IIB topoisomerases<sup>47</sup>). Both the fusion and the consolidation scenarios are speculative at best. In fact, phylogenetic analysis, as discussed below, points to independent origins for the type IIA topoisomerases in bacteria and eukaryotes.

Fourth, examination of the family tree yields no clear evolutionary pathway for the development of topoisomerase genes over time. For example, consider the following assessment by topoisomerase researchers regarding the evolutionary origins of these molecular machines:

“The phylogenetic distribution of DNA topoisomerases is thus *quite puzzling and clearly does not agree with the classical universal tree of life: neither with any of the alternative models such as the bacteria-first model nor with the ring of life model*. Another puzzling problem is the phylogenetic position of viral DNA topoisomerases. Whereas in some cases their placement can be explained by HGT [Horizontal Gene Transfer] from a cellular host (e.g. mimivirus Topo IA and IB), in other cases (e.g. Poxvirus Topo IB, T4 Topo IIA) the viral DNA topoisomerases form well-defined subfamilies that are only distantly related to their cellular counterparts [emphasis added].”<sup>3</sup>

Additionally, the recent discovery of the dimeric topoisomerase VIII in archaea and bacteria provides an additional example that does not fit well into evolutionary phylogenetics.

“This is therefore another example of a topoisomerase with an *unusual phylogenomic distribution and complex evolutionary trajectory* ... . Notably, bona fide topoisomerase VI enzymes present in bacteria cannot be distinguished from their archaeal homologs and branch with archaeal DNA topoisomerase VI enzymes in phylogenetic analyses; in contrast, topoisomerase VI and VIII enzymes are so divergent that their amino-acid sequences cannot be reliably aligned for phylogenetic analyses. It is *difficult to explain* why the fusion protein of the two topoisomerase VI-like subunits (i.e. the ancestor of topoisomerase VIII) would have diverged so rapidly in one particular bacterial lineage but remained conserved during its dispersion in various bacterial lineages [emphasis added].”<sup>47</sup>

In fact, the phylogenies are so incongruous that not only are there at least five proposed origins representing each of the classes (IA, IB, IC, IIA, IIB), but many of the members of the classes are proposed to have had independent

origins, particularly within the domains of life.<sup>3,8,45</sup> As noted above, each of these classes have highly similar mechanisms and protein structures. The implications of the similarities between the amino acid sequences are that these mechanisms and structures represent common designs used to solve the challenges associated with DNA topology. However, evolutionists conveniently rely on ‘convergent evolution’ to explain how ‘nature’ arrived at the same solution multiple times independently!

Further, one literature review on the evolution of topoisomerases suggests: “An intelligent designer would have probably invented only one ubiquitous Topo I and one ubiquitous Topo II to facilitate the task of future biochemists. The reality turned out to be quite different, and more interesting.”<sup>8</sup> What an interesting (and bold) claim: an intelligent designer would want to ‘facilitate the task of future biochemists’ and simplify the understanding of topoisomerases by only designing one of each type. This seems to miss the point that the various classes of topoisomerases that exist appear to be playing unique and distinct roles (though at times there is redundancy of function). In addition, multiple versions of these enzymes allow for more complex regulation of function. Perhaps it would be simpler from an evolutionary perspective if there were only two but the fact that there are multiple classes and subclasses suggests that organisms are far more complex than evolutionists want to admit. The sophistication and interdependence of cellular biochemistry provides excellent evidence for how “fearfully and wonderfully made” we truly are.

To explain the alleged evolution of these enzymes, evolutionists have relied on the unprovable assumption of (multiple) horizontal gene transfer events and the alleged existence of hypothetical ancestral versions of the enzyme that no longer exist.<sup>8</sup> Further, even if horizontal gene transfer did occur to spread some of these genes across organisms (which is likely in some of the viral and plasmid-encoded forms), it has no power to explain the *origin* of the first topoisomerase genes.

One of the most recent proposed scenarios for the evolution of topoisomerases involves a complex transition from an RNA genome to a DNA genome with topoisomerases evolving along the way.<sup>8</sup> This scenario again is purely hypothetical and lacks evidence. Further, it glosses over another major problem in evolutionary phylogenetics. Topoisomerases are not the only enzymes that do not fit neatly into ‘tree of life’ phylogenies. In fact, topoisomerases are joined by DNA polymerases and several other classes of enzymes and proteins that do not fit the phylogenies and have significantly altered the ‘tree of life’ concept.<sup>48,49</sup> In summary, topoisomerases represent a significant challenge

to evolutionary explanations of life, including abiogenesis and common ancestry.

## Summary

DNA topoisomerases are complex molecular machines with multiple interacting domains and coordinated mechanisms. These enzymes resolve topological challenges in our genomes on an ongoing basis throughout the cell cycle and even in non-dividing cells. Both replication and transcription cause topological strain that must be alleviated for the cell to survive. Further, chromosomes become interlinked during replication and must be decatenated for cells to survive. Topoisomerases resolve these problems using a transient, enzyme-linked single- or double-stranded DNA break. The double-strand break mechanism of the type II enzymes allows for these enzymes to cleave the DNA and pass an intact double helix through the break while protecting the cleaved ends from forming a permanent double-strand break.

Evolutionary explanations for the chance development of topoisomerases are severely lacking and fail to account for the critical nature of these enzymes in living systems. Further, the symmetry, domain organization, and overall coordination of topoisomerases support the concept that these enzymes are very well designed and are perfectly suited to carry out the tasks of maintaining the topological state of the genome. Further, while the temporary strand breaks generated by topoisomerases are potential threats to the genome, the enzyme protects the genome by its preferential ligation of cleaved DNA. What an amazing class of molecular machines these enzymes are! Topoisomerases truly are the intricate molecular scissors and ‘relaxers’ of the genome!

## Acknowledgements

I would like to express my appreciation to the numerous colleagues who have read and provided feedback on this manuscript. I also would like to thank my college and university for their support of my work.

## References

1. Watson, J.D. and Crick, F.H., Genetical implications of the structure of deoxyribonucleic acid, *Nature* **171**:964–967, 1953.
2. Deweese, J.E., Osheroff, M.A. and Osheroff, N., DNA topology and topoisomerases: teaching a ‘knotty’ subject, *BAMBED* **37**:2–10, 2009.
3. Forterre, P., Gribaldo, S., Gadelle, D. and Serre, M.C., Origin and evolution of DNA topoisomerases, *Biochimie* **89**:427–446, 2007.
4. Champoux, J.J., DNA topoisomerases: structure, function, and mechanism, *Annu. Rev. Biochem.* **70**:369–413, 2001.
5. Wang, J.C., Interaction between DNA and an Escherichia coli protein omega, *J. Mol. Biol.* **55**:523–533, 1971.



6. Wang, J.C., A journey in the world of DNA rings and beyond, *Annu. Rev. Biochem.* **78**:31–54, 2009.
7. Zhang, H., Barcelo, J.M., Lee, B. *et al.*, Human mitochondrial topoisomerase I, *Proc. Nat. Acad. Sci. USA* **98**:10608–10613, 2001.
8. Forterre, P. and Godelle, D., Phylogenomics of DNA topoisomerases: their origin and putative roles in the emergence of modern organisms, *Nucleic Acids Res.* **37**:679–692, 2009.
9. Zhang, H., Meng, L.H. and Pommier, Y., Mitochondrial topoisomerases and alternative splicing of the human TOP1mt gene, *Biochimie* **89**:474–481, 2007.
10. Nitiss, J.L., DNA topoisomerase II and its growing repertoire of biological functions, *Nat. Rev. Cancer* **9**:327–337, 2009.
11. Deweese, J.E. and Osheroff, N., The DNA cleavage reaction of topoisomerase II: wolf in sheep's clothing, *Nucleic Acids Res.* **37**:738–749, 2009.
12. Gubaev, A. and Klostermeier, D., The mechanism of negative DNA supercoiling: a cascade of DNA-induced conformational changes prepares gyrase for strand passage, *DNA Repair (Amst)* **16**:23–34, 2014.
13. Grue, P., Grasser, A., Sehested, M. *et al.*, Essential mitotic functions of DNA topoisomerase IIa are not adopted by topoisomerase II $\beta$  in human H69 cells, *J. Biol. Chem.* **273**:33660–33666, 1998.
14. Ju, B.G., Lunyak, V.V., Perissi, V. *et al.*, A topoisomerase II $\beta$ -mediated dsDNA break required for regulated transcription, *Science* **312**:1798–1802, 2006.
15. Linka, R.M., Porter, A.C., Volkov, A. *et al.*, C-terminal regions of topoisomerase IIa and II $\beta$  determine isoform-specific functioning of the enzymes in vivo, *Nucleic Acids Res.* **35**:3810–3822, 2007.
16. Cowell, I.G. and Austin, C.A., Mechanism of Generation of Therapy Related Leukemia in Response to Anti-Topoisomerase II Agents, *Int. J. Environ. Res. Public Health* **9**:2075–2091, 2012.
17. Heck, M.M. and Earnshaw, W.C., Topoisomerase II: A specific marker for cell proliferation, *J. Cell Biol.* **103**:2569–2581, 1986.
18. Hsiang, Y.H., Wu, H.Y. and Liu, L.F., Proliferation-dependent regulation of DNA topoisomerase II in cultured human cells, *Cancer Res.* **48**:3230–3235, 1988.
19. Woessner, R.D., Mattern, M.R., Mirabelli, C.K. *et al.*, Proliferation- and cell cycle-dependent differences in expression of the 170 kilodalton and 180 kilodalton forms of topoisomerase II in NIH-3T3 cells, *Cell Growth Differ.* **2**:209–214, 1991.
20. Isaacs, R.J., Davies, S.L., Sandri, M.I. *et al.*, Physiological regulation of eukaryotic topoisomerase II, *Biochim. Biophys. Acta* **1400**:121–137, 1998.
21. Austin, C.A. and Marsh, K.L., Eukaryotic DNA topoisomerase II $\beta$  *Bioessays* **20**: 215–226, 1998.
22. Tsutsui, K., Tsutsui, K., Okada, S. *et al.*, Molecular cloning of partial cDNAs for rat DNA topoisomerase II isoforms and their differential expression in brain development, *J. Biol. Chem.* **268**:19076–19083, 1993.
23. Watanabe, M., Tsutsui, K., Tsutsui, K. and Inoue, Y., Differential expressions of the topoisomerase IIa and II $\beta$  mRNAs in developing rat brain, *Neurosci. Res.* **19**:51–57, 1994.
24. Lyu, Y.L., Lin, C.P., Azarova, A.M. *et al.*, Role of topoisomerase II $\beta$  in the expression of developmentally regulated genes, *Mol. Cell. Biol.* **26**:792–7941, 2006.
25. McClendon, A.K., Gentry, A.C., Dickey, J.S. *et al.*, Bimodal recognition of DNA geometry by human topoisomerase II alpha: preferential relaxation of positively supercoiled DNA requires elements in the C-terminal domain, *Biochemistry* **47**:13169–13178, 2008.
26. French, S.L., Sikes, M.L., Hontz, R.D. *et al.*, Distinguishing the roles of topoisomerases I and II in relief of transcription-induced torsional stress in yeast rRNA genes, *Mol. Cell. Biol.* **31**:482–494, 2011.
27. Deming, P.B., Cistulli, C.A., Zhao, H. *et al.*, The human decatenation checkpoint, *Proc. Nat. Acad. Sci. U.S.A.* **98**:12044–12049, 2001.
28. Romanienko, P.J. and Camerini-Otero, R.D., Cloning, characterization, and localization of mouse and human SPO11, *Genomics* **61**:156–169, 1999.
29. Romanienko, P.J. and Camerini-Otero, R.D., The mouse Spo11 gene is required for meiotic chromosome synapsis, *Mol. Cell* **6**:975–987, 2000.
30. Bloomfield, G., Atypical ploidy cycles, Spo11, and the evolution of meiosis, *Semin. Cell Dev. Biol.* 2016.
31. Pommier, Y., Leo, E., Zhang, H. and Marchand, C., DNA topoisomerases and their poisoning by anticancer and antibacterial drugs, *Chem. Biol.* **17**:421–433, 2010.
32. Gibson, E.G. and Deweese, J.E., Covalent poisons of topoisomerase II, *Curr. Top. Pharm.* **17**:1–12, 2013.
33. Regal, K.M., Mercer, S.L. and Deweese, J.E., HU-331 is a catalytic inhibitor of topoisomerase IIa, *Chem. Res. Toxicol.* **27**:2044–2051, 2014.
34. Bates, A.D., Berger, J.M. and Maxwell, A., The ancestral role of ATP hydrolysis in type II topoisomerases: prevention of DNA double-strand breaks, *Nucleic Acids Res.* **39**:6327–6339, 2011.
35. Aravind, L., Leipe, D.D. and Koonin, E.V., Toprim—a conserved catalytic domain in type IA and II topoisomerases, DnaG-type primases, OLD family nucleases and RecR proteins, *Nucleic Acids Res.* **26**:4205–4213, 1998.
36. Schmidt, B.H., Burgin, A.B., Deweese, J.E. *et al.*, A novel and unified two-metal mechanism for DNA cleavage by type II and IA topoisomerases, *Nature* **465**: 641–644, 2010.
37. Bromberg, K.D., Hendricks, C., Burgin, A.B. and Osheroff, N., Human topoisomerase IIa possesses an intrinsic nucleic acid specificity for DNA ligation. Use of 5' covalently activated oligonucleotide substrates to study enzyme mechanism, *J. Biol. Chem.* **277**:31201–31206, 2002.
38. Wilstermann, A.M. and Osheroff, N., Positioning the 3'-DNA terminus for topoisomerase II-mediated religation, *J. Biol. Chem.* **276**:17727–17731, 2001.
39. Deweese, J.E. and Osheroff, N., Coordinating the two protomer active sites of human topoisomerase II: nicks as topoisomerase II poisons, *Biochemistry* **48**: 1439–1441, 2009.
40. Dong, K.C. and Berger, J.M., Structural basis for gate-DNA recognition and bending by type IIA topoisomerases, *Nature* **450**:1201–1205, 2007.
41. Deweese, J.E., Burgin, A.B. and Osheroff, N., Using 3'-bridging phosphorothiolates to isolate the forward DNA cleavage reaction of human topoisomerase IIa, *Biochemistry* **47**:4129–4140, 2008.
42. Schmidt, B.H., Osheroff, N. and Berger, J.M., Structure of a topoisomerase II-DNA-nucleotide complex reveals a new control mechanism for ATPase activity, *Nat. Struct. Mol. Biol.* **19**:1147–1154, 2012.
43. Baird, C.L., Harkins, T.T., Morris, S.K. and Lindsley, J.E., Topoisomerase II drives DNA transport by hydrolyzing one ATP, *Proc. Nat. Acad. Sci. U.S.A.* **96**:13685–13690, 1999.
44. Bjergbaek, L., Kingma, P., Nielsen, I.S. *et al.*, Communication between the ATPase and cleavage/religation domains of human topoisomerase IIa, *J. Biol. Chem.* **275**:13041–13048, 2000.
45. Godelle, D., Filee, J., Buhler, C. and Forterre, P., Phylogenomics of type II DNA topoisomerases, *Bioessays* **25**:232–242, 2003.
46. Fraser, C.M., Gocayne, J.D., White, O. *et al.*, The minimal gene complement of *Mycoplasma genitalium*, *Science* **270**:397–403, 1995.
47. Godelle, D., Krupovic, M., Raymann, K. *et al.*, DNA topoisomerase VIII: a novel subfamily of type IIB topoisomerases encoded by free or integrated plasmids in Archaea and Bacteria, *Nucleic Acids Res.* **42**:8578–8591, 2014.
48. Leipe, D.D., Aravind, L. and Koonin, E.V., Did DNA replication evolve twice independently?, *Nucleic Acids Res.* **27**:3389–3401, 1999.
49. Forterre, P., The two ages of the RNA world and the transition to the DNA world: a story of viruses and cells, *Biochimie* **87**:793–803, 2005.

**Joe Deweese** earned his B.S. in biochemistry (2004) from Freed-Hardeman University and his Ph.D. in biochemistry (2009) from Vanderbilt University School of Medicine. His laboratory research focuses on type II topoisomerases as anticancer targets and his work has been published in a number of peer-reviewed journals. He is an Associate Professor of Pharmaceutical Sciences within the College of Pharmacy and Health Sciences at Lipscomb University (Nashville, TN). He teaches biochemistry, cellular and molecular biology, and pharmacology to student pharmacists.

# The genetic effects of the population bottleneck associated with the Genesis Flood

Robert W. Carter and Matthew Powell

Skeptics familiar with the field of genetics claim the Creation/Flood/Babel model is unrealistic in terms of population genetics and demographics. To address these claims, we created a population modelling program designed to examine changes in allele frequency within 'biblical' populations. Our model included an artificial genome consisting of 100,000 alleles within 40 independent chromosome arms of variable length. We start with two individuals, set their alleles to a heterozygous state (to model 'created diversity'), and allow children to be born according to a set of predetermined population parameters. We control the average number of recombination events per chromosome arm per generation and track all alleles in all individuals. At a set year, we can introduce a 'Flood' by reducing the population to a single couple with three sons. Wives are assigned to these sons either by choosing randomly from available females in the population or by allowing the parental couple to produce three sisters. Population sizes of 100–500 individuals caused extreme levels of genetic drift and fixation, as expected, but these effects were minimal in populations between 4,000 and 50,000. The Flood had a demonstrable effect on reducing heterozygosity (due to inbreeding), but average fixation rates were low for moderate to large population sizes (an average of 0.76% loss with random wives, 3.07% if the wives are sisters to the parental couple's sons). After comparing to real-world allele frequency data, we conclude that the effective population size of humanity was at one point very small and that models with small antediluvian population sizes are more likely to reflect human history. The small early population size produced a significant amount of genetic drift in the original alleles and possibly led to a significant loss of created diversity. Thus, skeptical claims that biblical models are excluded by population genetics are unwarranted.

According to Genesis, humanity started with a single Adam from whose side a wife was produced (Genesis 1:27, 2:21–22). About 1,600 years later,<sup>1</sup> a flood destroyed the earth, leaving a single family with two parents, three sons, and three daughters-in-law (DILs) of unknown relation who went on to repopulate the earth (Genesis 7:7, 8:18–19). Later, a division of the population happened at Babel; from then on people spread across the globe (Genesis 11:1–9). What many people don't realize is that each of these events should have left a genetic signature on the modern population. Since the study of genetics is the study of how traits are passed from one generation to the next, science has given us specific tools to analyze population histories. We applied several of these tools to biblical population history.

There are several basic concepts that one must understand in order to deal with this subject. The first is called *genetic drift*. In small populations, random sampling of alleles each generation creates random changes in allele frequency. When populations stay small for many generations, extreme fluctuations in allele frequency can lead to allele *fixation*, where one allele is lost entirely and the other becomes fixed (i.e. 'stuck', not 'repaired').

The probability of an allele becoming fixed in the indefinite future is equal to the frequency of that allele in

the population divided by twice the population size (because humans are diploid):

$P_{\text{fix}} = f/2n$ , where  $f$  = the allele frequency and  $n$  = the population size.

Ignoring new mutations (which always enter the population at a frequency of  $1/2n$ ), common alleles can easily drift to fixation in small populations. It is a mathematical certainty, given enough time. However, drift is effectively silenced in a population after it reaches a few hundred members. It would take many generations for random drift to affect allele frequencies in large populations.

Another important concept is that of *created diversity*. There is no reason to expect that God created Adam and Eve with no built-in heterozygosity. This actually answers a challenge issued by several critics, specifically Francis Collins, who said:

"There is no way you can develop this level of variation between us from one or two ancestors,"<sup>2</sup> and his *Biologos*<sup>3</sup> fellow, Dennis Venema, who said:

"You would have to postulate that there's been this absolutely astronomical mutation rate that has produced all these new variants in an incredibly short period of time. Those types of mutation rates are just not possible. It would mutate us out of existence."<sup>4</sup>

Both of their conclusions represent a superficial approach to biblical genetics. While it is true that mutation rates of that magnitude would kill us, it is only true if we have to explain all of human genetic diversity as a product of mutation. They completely ignore God-created diversity. But how much created diversity should we expect? There are about 10 million places in the human genome with two alleles ('bi-allelic SNPs') where both alleles are found in all major world populations.<sup>5</sup> Since it is statistically impossible to account for these through parallel mutation, these must have existed at Babel—therefore they were on the Ark, therefore they were in Eden. If these are new mutations, they must have arisen in multiple populations independently. The statistical impossibility of this is the basis of the 'Out of Africa' model of human origins that posits modern humans rose from a single source population.<sup>6</sup> The commonality of millions of alleles across world populations is the major reason modern geneticists have rejected all earlier views on the origin of races. As the well-known geneticist Lluís Quintana-Murci recently said:

"But the genes that explain the phenotypic differences between populations only represent a tiny part of our genome, confirming once again that the concept of 'race' from a genetic standpoint has been abolished."<sup>7</sup>

There is also an additional unknown number of new mutations within the human genome. With a human population size of seven billion, it might be expected that every survivable mutation currently exists, but you would need to sequence the genomes of all seven billion people to find them. However, the less common a variation is, the more likely it is of recent origin (i.e. a mutation). Common variants occurring across populations are good candidates for created diversity, and rare variants that appear in a single population, tribe, or individual are good candidates for new mutations. We can therefore discount the rare variants without sacrificing created diversity.

The average human carries 4–5 million heterozygous alleles,<sup>8</sup> with Africans generally having higher levels.<sup>9</sup> Is it reasonable to assume the majority of these alleles were placed by God into Adam and/or Eve? Would not most of that initial created diversity have been lost at the Flood? How much drift and/or fixation would one expect in a Creation/Flood/Babel scenario? Would not the inbreeding of the three post-Flood families drive humanity to extinction? Should we expect genetic homogeneity among the descendants of the Flood survivors, and is not the lack of homogeneity proof that the Flood never happened? We can answer each of these questions directly using computer programs that incorporate real-world rates for various genetic phenomena (mutation, chromosomal recombination, etc.).

**Table 1:** Population input parameters

Parameter	Default values	Value ranges used in this paper
Number of iterations	100	10 to 100
Years per iteration	6,000	100 to 6,000
Max. population size	10,000	100 to 50,000
Av. # recombinations/arm/gen.	1	0 to 3
Save interval (years)	100	100
Year of bottleneck	1,600	1,600
Force-related DILs	False	True, false
Age of maturity	20	15 to 25
Maximum lifespan	900	900
Pre-bottleneck lifespan factor	0.98	0.98
Post-bottleneck lifespan factor	0.7	0.7
Minimum lifespan	120	120
Probability of birth per year	1/3	1 to 1/3
Minimum child spacing	3	1 to 10
Pre-bottleneck spacing factor	1	1
Post-bottleneck spacing factor	0.9	0.9
Age of senescence	400	400
Post-bottleneck senescence factor	0.333	0.333

**Table 2:** Structure of the modelled genome

Arm length (number of alleles)	Number of arms at that length
5,000	4
4,000	6
3,000	8
2,000	10
1,000	12
Total: 100,000	Total: 40

Carter and Hardy created a model designed to test various models of population growth and applied it to the questions of pre-Flood, pre-Babel, and post-Exodus population sizes.<sup>10</sup> They concluded early births are the most important factor controlling population growth. Long-lived patriarchs were basically irrelevant, because the contribution of a child to the future population is inversely proportional to the population size when the child is born. Having children late in life has little effect on the future population size. Their conclusions



were important for the development of the model we will describe in this paper.

In *The non-mythical Adam and Eve*,<sup>11</sup> Carter tackled claims made by Collins and Venema, who not only do not believe Adam and Eve were real historical figures but believe Adam and Eve are impossible based on what we know about human genetics. He concluded their criticisms were both unwarranted and displayed a shallow understanding of basic biblical concepts. Starting with Adam and Eve, genetic drift over time would have created an allele frequency spectrum similar to what we see today. Also, the threat of allele loss through fixation would be minimal.

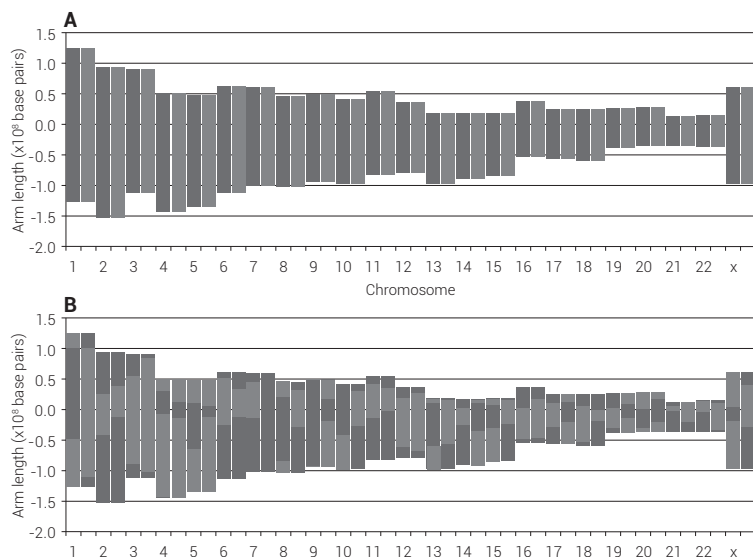
But Carter's model was overly simple. He used only 1,000 alleles, and alleles were inherited independently (i.e. no 'linkage'). When we took that model and divided the alleles into ten distinct blocks (a simple model of chromosome arms), the results obtained were quite different. Many more alleles were lost to drift and fixation. This precipitated the current study. We simply wanted to better understand a basic question: does a Creation/Flood/Babel model reflect modern human population genetics?

## Methods

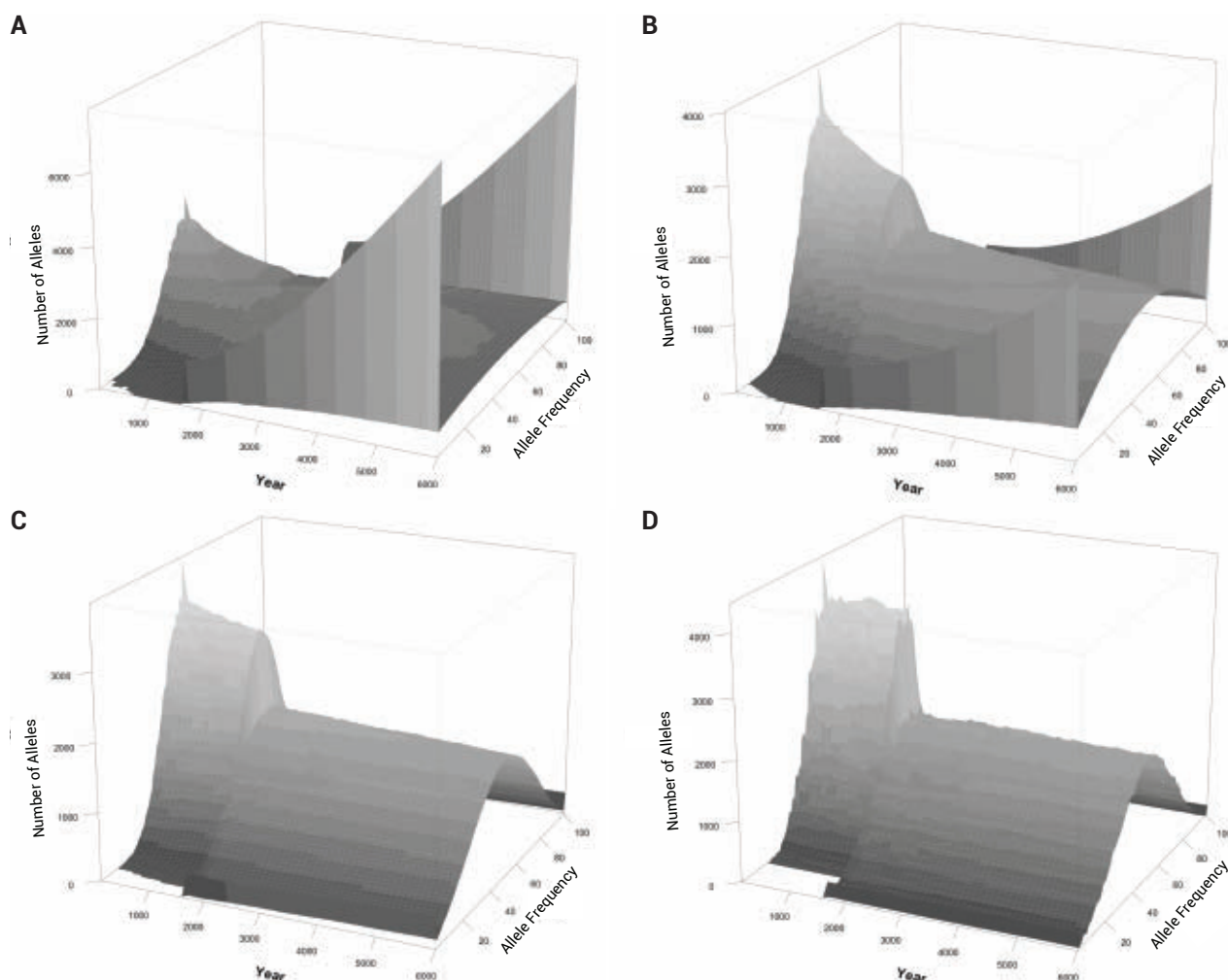
After prototyping a population model in Perl, then more advanced models in R, we implemented a full version in C for vastly improved speed and memory usage, reserving R for graphics and some data processing. We created several virtual instances on the Amazon Web Services (AWS) cloud and ran the models in bulk. An individual model takes various input parameters (table 1), based on previous work.<sup>10</sup> We created an artificial genome by assigning 100,000 alleles to forty recombining 'chromosome arms', ranging in size from 1,000 to 5,000 alleles, paralleling on a reduced scale the allele density per chromosome arm in the HapMap<sup>12</sup> data. Even though there are millions of segregating alleles in the human genome, 100,000 markers gives enough data density to see the effects of recombination in the modelled populations over many generations. Essentially, we struck a compromise between computational time and the need for more markers than the projected number of recombination events per run. Due to high levels of recombination within the centromere every generation,<sup>13</sup> the chromosome arms are essentially independent units and the acrocentric chromosomes do not have two distinct arms. Thus there are about forty

recombining units in the genome and our allele density parallels that of real human chromosomes (table 2).

Each model run starts with two individuals. We create two bitmaps with 100,000 columns and  $n$  rows, where  $n$  = a preset maximum population size. The bits in one bitmap are set to 1 for Adam and 0 for Eve, with the other bitmap arbitrarily initialized in the inverse way. Since each row represents one copy of one individual's genome, we essentially start with 100,000 biallelic loci (more technically called 'single nucleotide polymorphisms', or SNPs). During each time step ('years'), children are born, men and women marry, and old people die. Child genomes are created by taking the two genomes of each parent and randomly choosing crossover points along each modelled chromosome arm. One recombined haploid genome is passed to the child from each parent. For each chromosome arm, we randomly select between the two versions carried by the parent, copy the alleles from that chromosome up to the point of crossover, then switch to the other chromosome. For models that allow greater than one crossover per arm per generation, the algorithm simply switches to the other parental copy at each calculated crossover point. Iterating in this way through all chromosome arms and combining



**Figure 1.** Example recombination in a representative female genome. The chromosomes in this example are lined up on the centromere ('0' on the y-axis), with arms of various lengths. The shorter p arms are assigned positive lengths and the longer q arms negative lengths. (A) An example parental genome. Both parents start with two copies of each chromosome (dark and light grey). One crossover point is chosen at random along each chromosome arm and the light and dark grey copies are recombined. (B) A child, in this case a female, inherits recombined chromosomes from both parents, leading to a patchwork pattern of inheritance with every generational step. For each chromosome pair, the first is the (recombined) chromosome inherited from the father; the second is from the mother.



**Figure 2:** 3-D allele frequency histogram for four example model runs with a Flood bottleneck at year 1,600: a)  $n = 500$ , b)  $n = 1,000$ , c)  $n = 5,000$ , d)  $n = 50,000$ . The Flood bottleneck clearly had an effect on the allele distribution, but did not elevate fixation rate in the larger population sizes.

the results from each parent creates a diploid child genome (figure 1).

In order to simulate specific population sizes and keep computer processing and memory requirements to a reasonable level, we set a maximum population size. After reaching that predetermined size, new births caused the death of a random individual (other than the parents) already in the population. Under the standard parameters, about 5% of the individuals were replaced every year. This seems high, but the only other options were to allow the population to continue growing to infinity, to introduce controlled randomized death and/or population reduction events based on assumed causes, or keep the birth rate to levels that are unrealistically low.

To compare our results to those of real-world populations, we downloaded the most recent (Phase II, build 36), forward strand, non-redundant allele frequency statistics for three major world populations from HapMap.org.<sup>14</sup> Populations

were CEU (individuals of northern and western European descent living in Utah), YRI (Yorubas from Nigeria), and CHB+JPT (Chinese living in Beijing and Japan). After filtering to include only those variants that appeared in all three populations, data for over 3.6 million biallelic loci were obtained. For each population, the frequency of the major and minor alleles was calculated for each locus and the allele frequencies were summed and binned in intervals of 0.01.

## Results

Figure 2 displays the allele frequency data for several model populations, averaged over 100 model runs (only 10 runs for  $n = 50,000$ ). Population sizes were: a) 500, b) 1,000, c) 5,000, d) 50,000. A Flood-type bottleneck with random DILs occurred at year 1,600. The two wings that appear in later years among the smaller populations represent alleles that drifted to fixation (0% or 100%). There was almost no

noticeable difference between the populations with 5,000 to 50,000 individuals, meaning we successfully captured the size range required to draw conclusions about any larger population size.

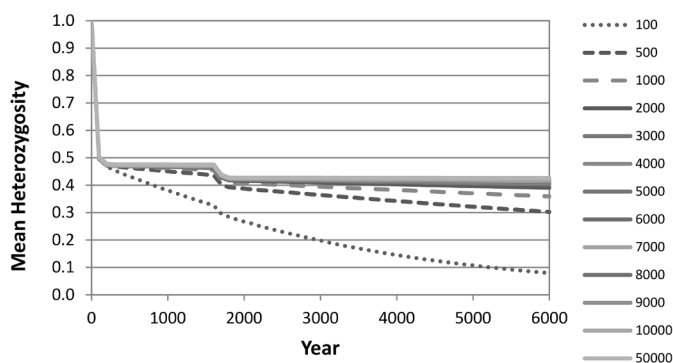
Changes in average population-wide heterozygosity in models with different maximum population sizes are shown in figure 3. When the population size was  $\geq 3,000$ , heterozygosity levels were consistent and similar, and most of the loss occurred when the population was rebounding from small numbers. The average loss of heterozygosity from the Flood year to the next measurement period (100 years after the Flood) in the smallest population was 9.4%. Loss of heterozygosity in all other populations was similar, averaging 7.5%. By the time the population reached 50,000 people, the average heterozygosity had levelled out to a value of 0.427 and had not changed (to three significant figures) in 1,300 years. The slope of that line over the final 2,000 years was  $-3 \times 10^{-7}$ , meaning we would expect a  $-0.03\%$  change over the next 1,000 years.

We compare the allele frequency spectrum for multiple population sizes at model year 6,000 in figure 4. As above, the larger population sizes begin to converge. In this case, a normally distributed curve centred on 0.5 was obtained. Since all alleles started at a frequency of 0.5, and since drift was expected to create variation in the allele frequencies, this was a good demonstration that our methods were producing realistic results. Models that restricted the population to less than 1,000 people had appreciable allele loss (fixation). All other populations exhibited a more-or-less normal distribution, with only slight levels of fixation.

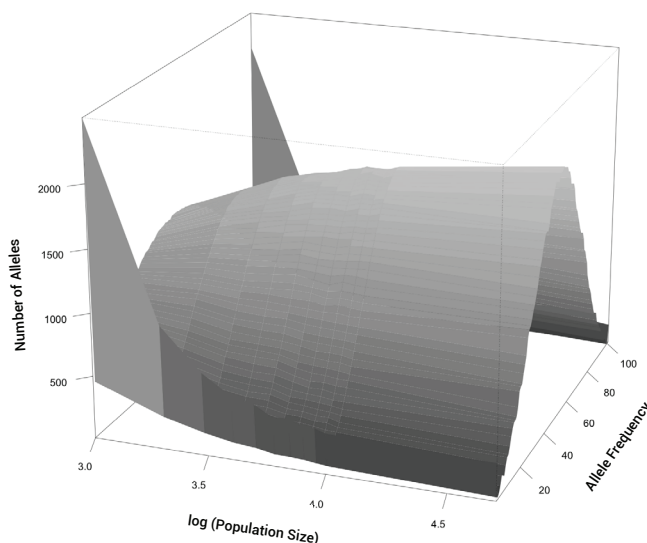
We also tested what would happen with two extreme models: one with the DILs pulled at random from the available females at the time of the Flood and one with the DILs as sisters of Shem, Ham, and Japheth. Data were taken from an average of 100 iterations for each population size of 100, 500 and 1,000 to 10,000 and 10 iterations for a population size of 50,000. We calculated the difference in mean heterozygosity between the 1,600<sup>th</sup> year, just prior to the flood event, and the 1,700<sup>th</sup> year, 100 years after the event (figure 5). Note that for the algorithm to work in small populations where it was rarely possible to find a ‘Noah’ with 6 children, some new sons and their wives had to be created during the Flood event. This figure shows an average reduction of 7.8% (for random DILs) or 16.1% (for sibling DILs) in mean heterozygosity, irrespective of population size. Figure 6 displays the allele frequency spectrum of the two modelled populations. The two ‘wings’ on each graph represent alleles that have gone to fixation

(at 0% or 100% allele frequency). The models with random DILs lost 0.76% of the alleles, on average, due to fixation for population sizes between 4,000 and 50,000. In the model where the DILs were daughters of Noah, 3.07% of the alleles were lost to fixation for those same population sizes (400% higher, but still modest). We were also able to compare heterozygosity and fixation for these models (figure 7).

Since most of the loss in heterozygosity occurred when the population was small, we created models with varying population growth rates and tracked the allele frequency



**Figure 3.** Average population-wide heterozygosity for model runs with various maximum population sizes. Adam and Eve, by definition in this model, have a heterozygosity of 1.0. Because each child will inherit multiple identical chromosomal sections from the two parents, none of the 1st-generation children are nearly as heterozygous as the first couple. For the larger populations, note how the majority of loss occurred in the first few generations from Adam and Eve, then again from Noah. Also, note how the steady-state slope for the larger population sizes approaches zero very quickly, meaning there is only a little loss of heterozygosity.



**Figure 4.** Allele frequency distribution at year 6,000 for populations of various maximum sizes. Data taken from an average of 100 (except for max. population size 50,000 with 10) iterations in a model with default population parameters.



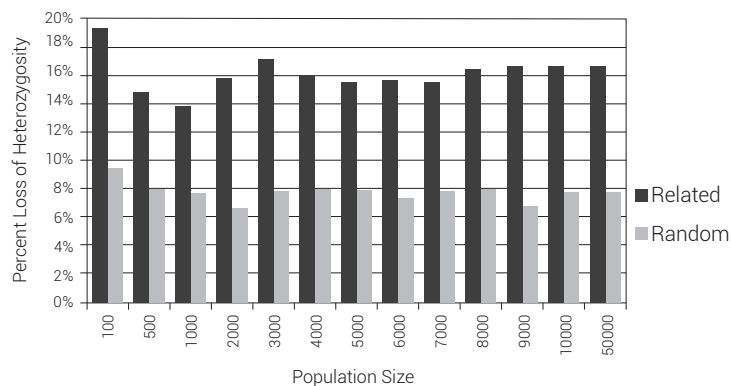
spectrum for 500 model years (figure 8). Fast growth led to less drift (a tighter allele frequency distribution). Slower growth created a flatter, wider curve, meaning more alleles had drifted away from their 50% starting point. In the slowest-growing population (S10/M25) it took a little less than 400 years to reach 10,000 people. This is slow compared to biological realities, so we feel the range of variables in these models span what we might expect to occur in the real world.

We also tested the effects of chromosome arm length on fixation and the retention of heterozygosity. No differences were found, to three significant figures, in either measure (data not shown). In order to assess the effects of recombination rate, we created models with a variable number of recombinations per arm per generation. With no recombination the allele frequency spectrum was quite erratic because there were essentially only 80

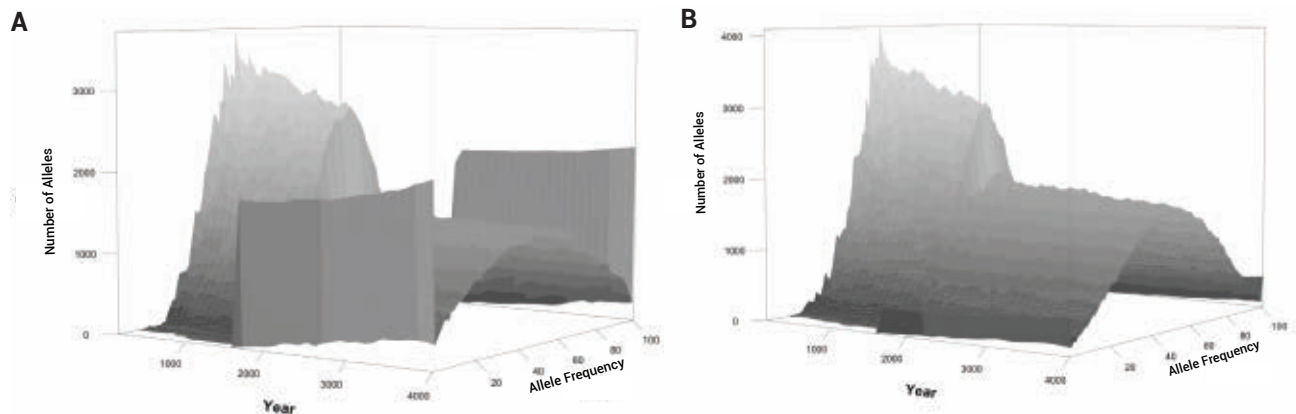
different alleles in the population, each at a different specific frequency (figure 9).

The allele frequency data for three major world populations is given in figure 10. In all three populations there are many alleles at both high and low frequencies, consistent with significant levels of drift. The average heterozygosity across the populations was 30.2%, consistent with the values generated at lower population sizes in our computer model (figure 3). It is not possible to measure fixation with these data, however, for HapMap would have skipped over any location that displays no allelic variation within, or among, contemporary populations. Figure 11 plots the relative difference for each of the 1.3 million HapMap alleles in two populations (CHB+JPT and YRI) compared to CEU. The difference in allele frequency between the European population and one of the other populations is shown along each axis. From this figure, we can see that the frequency of an allele in one population is

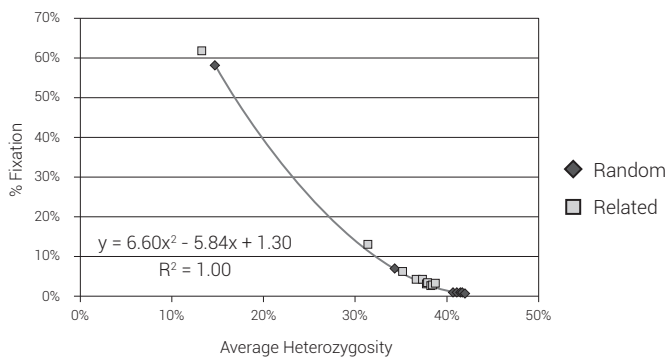
an excellent predictor of the frequency in the other two populations. If these were created alleles, a significant amount of drift must have occurred to drive them from their expected starting frequency of 50%. Yet, since the frequency of an allele in one population is a general predictor of the frequency in another population, this is an indication that the alleles took on this frequency spectrum prior to the separation of the populations at Babel. Subsequent within-population drift caused the widening of the distribution, but note how minimal this is. The slight ridge along the JPT+CHB axis represents alleles that drifted in this population but not the other two. The dual ridge that lies on the diagonal represents alleles that drifted in the CEU population and not the others.



**Figure 5.** Comparative loss of population heterozygosity during a flood event for random and related DILs. The height of the bars indicates the percent difference in mean heterozygosity between the 1,600th year, just prior to the Flood event, and the 1,700th year, 100 years after the event. Error bars not shown.



**Figure 6.** Allele frequency spectrum after 4,000 years for a model with related (A) and random (B) DILs with a maximum population size of 2,000 individuals. Data taken from an average of 10 iterations for both models. Clearly, the degree of relatedness of the DILs has a profound influence on the future population.



**Figure 7.** The relationship between heterozygosity and fixation for models with different population sizes and with related (open squares) and random (filled diamonds) DILs. Smaller populations are on the top left. Also included is a polynomial regression line for the random DILs. The degree of allele loss through fixation is inversely proportional to population heterozygosity. Thus, it may be possible in future models to estimate how many 'created' alleles were lost to drift based on modern human heterozygosity values (the three HapMap populations used in this study averaged 30.2% heterozygosity across the over 1 million sites included in the database).

## Discussion

We have demonstrated that a biblical population model can well account for what we see in the modern human population. In an article titled *The Search for the Historical Adam* that appeared in *Christianity Today*, the author states:

"In a recent pro-evolution book from InterVarsity Press, *The Language of Science and Faith*, [Francis] Collins and co-author Karl W. Giberson escalate matters, announcing that 'unfortunately' the concepts of Adam and Eve as the literal first couple and the ancestors of all humans simply 'do not fit the evidence'."<sup>15</sup>

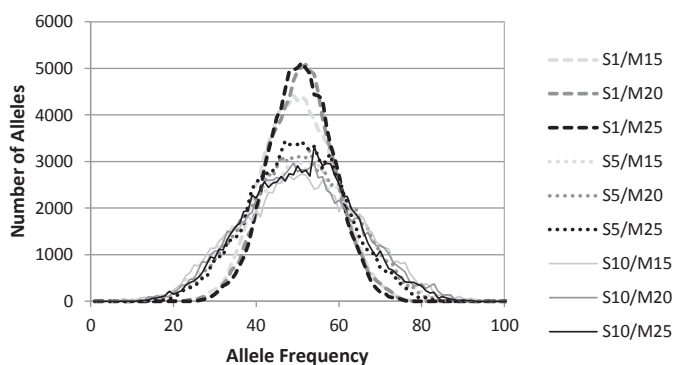
We wonder exactly what evidence they are leaning on to draw these conclusions, for this study has shown that Adam and Eve can, in fact, explain the evidence we see. There is no reason to reject the biblical account based on the number of alleles in the modern human population, the distribution of those alleles, or the supposed genetic risk-factors associated with the biblical Flood.

This does not mean there is no more work to be done. Far from it, in fact. For example, our realistic population models were unable to determine the degree of loss of allelic diversity in a Creation/Flood/Babel scenario. Since we do not know ancient human demographic history, we cannot, with certainty, say what happened to the original genes God put into Adam and Eve. However, this does not mean that modelling a range of potential options is a useless endeavor. In fact, after performing this analysis we have a much better understanding of how to explain

the allelic diversity found among people today. Is it unfair of us to appeal to a limited set of explanatory models when trying to fit the data to biblical history? Hardly, for this is exactly how the Out of Africa theory developed<sup>16</sup> and it is still common practice among evolutionists today.<sup>17</sup>

The idea that inbreeding depression would be a significant risk factor for human extinction is now moot. When we consider the number of common alleles circulating among living people, and the fact that the great majority of these are phenotypically neutral, it is not a stretch to conclude Adam and Eve carried about 10 million or more heterozygous loci and that nearly all of these have been retained in the modern human population. This depends on how many would be expected to be lost to fixation, which we estimate to be greater than 3% (the amount lost in medium to large model populations).

Genetic drift has certainly occurred, to the point where the original allele distribution has been flattened. The effect of all this drift is to make the allele frequency distribution almost appear as if the population is in mutation-drift equilibrium. This is a theoretical point at which mutations are entering the population at the same rate at which they are being removed by genetic drift, creating an allele frequency curve with many rare mutations. In other words, it is difficult to distinguish the biblical model from the evolutionary model as far as allele frequencies are concerned. What we see in contemporary humans is exactly what we would expect from an inbred or historically small population, and there is abundant opportunity for inbreeding: 1) among the ancestors of the Ark passengers prior to the Flood, 2) among the three post-Flood couples, 3)



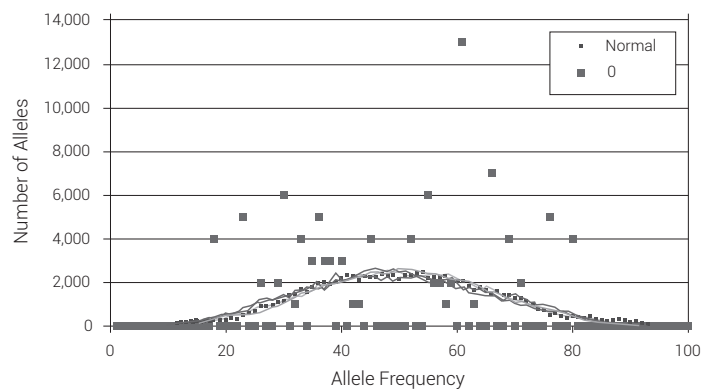
**Figure 8.** The effects of population growth rate. By varying the spacing of children ('S') from 1 to 10 years, and by varying the year of maturity for females ('M') from 15 to 25 years, we can affect the allele frequency distribution. Clearly, faster population growth slows genetic drift. Shown here are the average distributions after the first 500 years. There are only 10 model runs per variable, so the curves are not as smooth as in the other figures.

among the pre-Babel people, and 4) within the many post-Flood people groups.<sup>18</sup> We feel the best candidate timeframe for the necessary inbreeding is that of the pre-Flood to Flood people, because there is not much time between the Flood and Babel, and because the Bible records rapid post-Flood population growth.

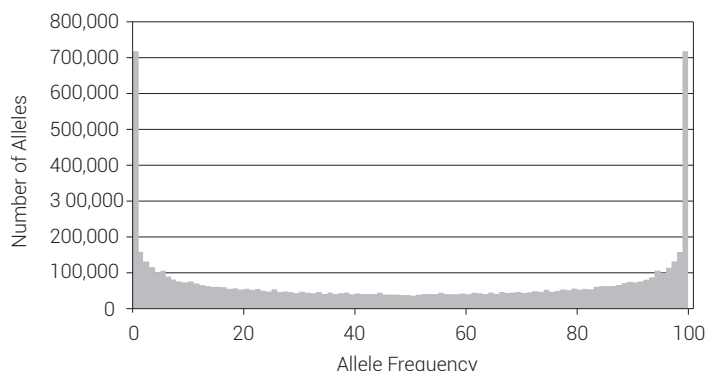
There is one other consideration to make before we conclude the discussion of created diversity, however: the introduction of mutations to the population prior to Babel. Most new mutations are expected to be lost to drift,<sup>19</sup> but we have shown that drift of existing, high frequency alleles slows dramatically in exponentially growing populations. Mutational load in children increases with the age of the father (due to the fact that older men pass on gametes that have gone through many more generations/genome copying events than younger men). Thus, any child born to an ancient person could theoretically carry many genetic differences from other people. Extrapolating from the data of Crow,<sup>20</sup> a man 500 years of age would donate approximately 10,000 mutations to a child (the current average is two orders of magnitude less than that). Kong *et al.* concluded that every extra year of paternity adds an average of about 2 additional mutations.<sup>21</sup> This would mean Noah would only contribute slightly more than 1,000 mutations (40 baseline mutations + 500 years x 2) after age 500. But they also discuss models with an exponential mutational increase over time and only studied men under age 50. Either way, it could be said that Noah, by far the oldest to have fathered children recorded in biblical history, was ‘genetic poison’ to the future world population, as he would be expected to have contributed many new mutations to each of his three sons (and possibly his daughters-in-law, if they were daughters). Even though many of these alleles would have been lost to drift in the early post-Flood years, many could still exist today but most would appear as rare alleles in the mutation spectrum. This alone might explain the preponderance of alleles in the 0–1% category in figure 10. This will also be the subject of future modelling efforts.

There has been some confusion in the literature concerning created diversity and mutation. For example, Williams attributed the allelic diversity in modern humans to mutation, and perhaps conflated ‘deleterious SNPs’ with allelic diversity in general, failing to note that the bulk of common variation is phenotypically neutral and not measurably deleterious. *Rare* variants are more likely to be harmful (the major conclusion of the paper he

cites<sup>22</sup>). He concluded, “It seems reasonable therefore to assume that something like 3 million of our SNPs have accumulated since creation”, but he derived this number by multiplying total allelic diversity (not rare allelic diversity), by the fraction calculated to be deleterious.<sup>23</sup> He clarified things in a subsequent paper,<sup>24</sup> but left open the possibility for a massive introduction of new mutations at or around the time of the Flood. This is an interesting possibility, but since there are only a few generations between the Flood and Babel and since recombination occurs in large chunks each generation, it would be difficult to spread millions of mutations thoroughly enough in the pre-Babel population so that they would be found in the multiple post-Babel tribes,



**Figure 9.** The effects of varying recombination rate. These are the allele frequency distributions at model year 1,500 for six populations. The results are not averaged. Only one run per population is shown. ‘Normal’ is the model with default settings and includes an average of 1 recombination per chromosome arm per generation. ‘0’ is a model with no recombination (*p* and *q* arms were inherited randomly, however). The other models (0.5, 2, and 3 recombination events per chromosome arm per generation) are represented by the thin lines covered by the ‘normal’ points. Even a small amount of recombination is enough to prevent random swings in allele frequency.



**Figure 10.** Combined allele frequency histogram data for three major world populations (Europeans, East Asians and Central Africans). Note that the two sides are mirror images, because for every allele at frequency *n* there is always a corresponding alternate allele at frequency 1-*n* (e.g. 0–1% equals 99–100%, etc.). There are many alleles at both high and low frequencies, but there are not many alleles in the middle range. This informs us of human demographic history, but the final distribution depends on many factors.



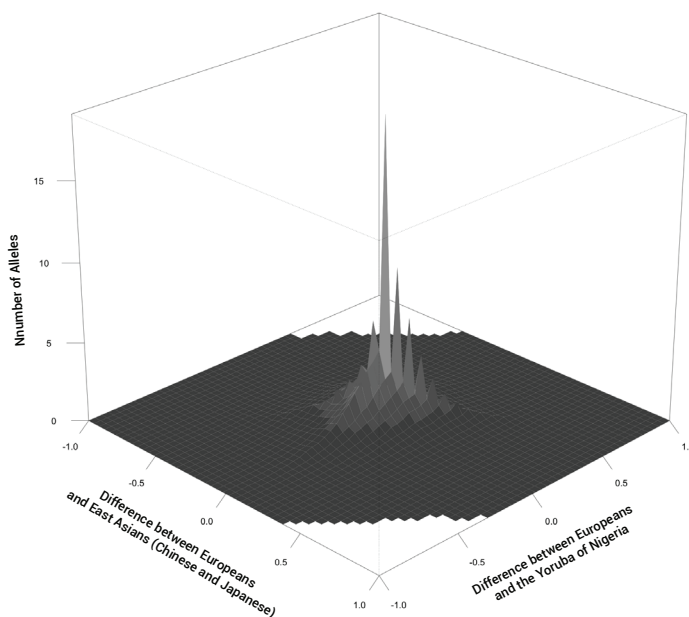
unless they occurred very early (e.g. in Noah). This is calling for more study!

What do our conclusions mean for the rapid decline in human lifespan after the Flood? A strong bottleneck could produce a situation in which ‘longevity’ genes could be lost, as Wieland suggested.<sup>25</sup> Since nearly all new mutations are lost to drift,<sup>26</sup> there is little chance that a deleterious allele (or alleles) that affected lifespan was fixed in the post-Flood population. Others have demonstrated that the lifespan decline follows a tight biological decay curve and it is entirely unlikely that the author of Genesis made up numbers that so clearly represent something biological that was happening to the individuals in that population. We now know that there are multiple factors that control lifespan in humans, and people that carry significantly more of these factors tend to live significantly longer than average, even though they carry the same variants that cause disease and death in other individuals.<sup>27</sup> There also exist areas with a significantly greater number of centenarians than average, for example people living in the highlands of Sardinia,<sup>28</sup> the genetics of whom also happen to be associated with the original settlers on the island.<sup>29</sup> Somehow, the loss of a certain amount of created diversity, the accumulation of new and deleterious mutations, the loss of heterozygosity in general, changes in the environment, and a likely change in epigenetic factors led to a significant decrease in human lifespan. This subject is calling for further critical inquiry.

One might wonder why we did not use an already available computer program for this project. Obviously, evolutionary population genetics programs are ill-suited to studying creation scenarios. The most comprehensive population genetics modelling program, Mendel’s Accountant,<sup>21</sup> was written by creationists in order to address specific evolutionary claims. It has been used to measure the rate of mutation accumulation in natural populations<sup>30</sup> and the power of natural selection (even pegging the selection coefficient for the first time ever<sup>31</sup>). Yet, ‘Mendel’ uses discrete generations: at each time interval all adults die and are replaced by their progeny. This is acceptable for large populations, but in a Creation model we need to reduce the population to small numbers with overlapping generations and so we needed to develop a platform that could handle these specific requirements. Preliminary results from an updated Mendel’s Accountant that can better model a Flood bottleneck look promising, but the update was not yet published as of the time of writing.

From the results of work done elsewhere by Carter (data not shown), chromosome arms might have 0, 1, 2, or more clear recombinations per generation, and recombinations average just over 65 per individual, per generation. Recombination is a well-known and well-characterized phenomenon controlled by the PRDM9 gene, which targets specific signal motifs in the genome.<sup>32</sup> These motifs can degrade through mutation. It is also known that recombination rates vary across the genome and among different groups of people.<sup>33</sup> Thus, a more detailed model that includes different rates of recombination in time- or genome-space might be able to answer questions about the difference between Africans and non-Africans, for example. But we will leave this to others and will freely share our population model (in C) upon request.<sup>34</sup>

We have established that our model produces results consistent with classic population genetics theory and that it can be used to explore alternate hypotheses of human demographic history. We believe that a small antediluvian population will create much genetic drift, and if this is followed by an exponential post-Flood growth phase, the allele frequencies will be frozen in place. Also, we would like to incorporate *de novo* mutations. It is quite likely that the majority of alleles in the 0–1% and 99–100% categories



**Figure 11.** 3-D histogram of the relative difference in allele frequency for each of the 1.3 million HapMap alleles in two populations (East Asians and Central Africans) compared to those in Europeans. Along each horizontal axis is the relative difference in allele frequency between Europeans and one of the other populations. The z axis gives the number of alleles at that frequency. The central peak is due to the fact that most alleles are at approximately the same frequency in all three populations (i.e. the difference between Europeans and each of the others is close to 0). This is a strong indication that the allele frequency spectrum was set up prior to the separation of the populations at Babel.

in figure 10 are due to pre-Babel mutations that were captured by the subsequent population growth.

## References

- Hardy, C. and Carter, R., The biblical minimum and maximum age of the earth, *J. Creation* **28**(2):89–96, 2014.
- Francis Collins speaking at the Christian Scholars' Conference at Pepperdine University, 2011; see "Noted scientist tackles question of religious faith", *Malibu Times*, 29 June 2011; malibutimes.com/articles/2011/06/29/news/news5.txt.
- Cosner, L., Evolutionary syncretism: a critique of Biologos, 7 September 2010, creation.com/biologos-evolutionary-syncretism.
- Haggerty, B.B., Evangelicals question the existence of Adam and Eve, National Public Radio, 9 August 2011; npr.org/2011/08/09/138957812/evangelicals-question-the-existence-of-adam-and-eve?ft=1&f=1001.
- Frazer, K.A. *et al.*, A second generation human haplotype of over 3.1 million SNPs, *Nature* **449**:851–862, 2007.
- Carter, R., The Neutral Model of evolution and recent African origins, *J. Creation* **23**(1):70–77, 2009; creation.com/neutral-model-of-evolution-recent-african-origins.
- Quintana-Murci, L., National Centre for Scientific Research (France), Human variation chalked up to natural selection: study, PhysOrg.com, 4 Feb 2008; physorg.com/news121369077.html.
- The 1000 Genomes Project Consortium, A global reference for human genetic variation. *Nature* **526**:68–77, 2015.
- Tiskoff, S.A. *et al.*, The genetic structure and history of Africans and African Americans, *Science* **324**(5930):1035–1044, 2009.
- Carter, R. and Hardy, C., Modelling biblical human population growth, *J. Creation* **29**(1):72–79, 2015.
- Carter, R., The non-mythical Adam and Eve: Refuting errors by Francis Collins and BioLogos, 20 August 2011, creation.com/historical-adam-biologos.
- The International HapMap 3 Consortium, Integrating common and rare genetic variation in diverse human populations, *Nature* **467**:52–58, 2010; www.hapmap.org.
- Jaco, I. *et al.*, Centromere mitotic recombination in mammalian cells, *J. Cell Biol.* **181**(6):885–892, 2008.
- ftp://ftp.ncbi.nlm.nih.gov/hapmap/frequencies/latest\_phaseII\_ncbi\_b36/fwd\_strand/non-redundant/.
- Ostling, R.N., The Search for the Historical Adam, *Christianity Today*, 3 June 2011, pp. 23–24.
- Carter, R., The Neutral Model of evolution and recent African origins, *J. Creation*, **23**(1):70–77, 2009; creation.com/neutral-model-of-evolution-recent-african-origins.
- Henn, B.M. *et al.*, Distance from sub-Saharan Africa predicts mutational load in diverse human genomes, *Proc. Natl. Acad. Sci. (USA)*, 2015; pnas.org/cgi/doi/10.1073/pnas.1510805112.
- Carter, R., Inbreeding and the origin of races, *J. Creation* **27**(3):8–10, 2013; creation.com/inbreeding-and-origin-of-races.
- Sanford, J.C. *et al.*, Mendel's Accountant: a biologically realistic forward-time population genetics program, *Scalable Computing: Practice and Experience* **8**(2): 147–165, 2007.
- Crow, J.F., The origins, patterns and implications of human spontaneous mutation, *Nature Reviews Genetics* **1**:40–47, 2000.
- Kong, A. *et al.*, Rate of de novo mutations, father's age, and disease risk, *Nature* **488**(7412): 471–475, 2012.
- Fu, W.-Q. *et al.*, Analysis of 6,515 exomes reveals the recent origin of most human protein-coding variants, *Nature* **493**(7431):216–220, 2013 | doi:10.1038/nature11690. Note also that if most common variants are part of created diversity, and rare variants are more likely to cause disease, this suggests that new mutations are more deleterious than evolutionists would generally like to admit.
- Williams, A., Human genome decay and the origin of life, *J. Creation* **28**(1): 91–97, 2014; creation.com/human-genome-decay-and-origin-of-life.
- Williams, A., Healthy genomes require recent creation, *J. Creation* **29**(2):70–77, 2015.
- Wieland, C., Decreased lifespans: Have we been looking in the right place? *J. Creation* **8**(2):138–141, 1994; creation.com/decreased-lifespans-have-we-been-looking-in-the-right-place.
- Rupe, C.L. and Sanford, J.C., Using numerical simulation to better understand fixation rates, and establishment of a new principle: Haldane's Ratchet, *Proceedings of the Seventh International Conference on Creationism*, Harsh, B., Ed., Creation Science Fellowship, Pittsburg, PA, 2013.
- Sebastiani, P. *et al.*, Genetic Signatures of Exceptional Longevity in Humans, *Science Express* 0.1126/science.1190532, 1 July 2010.
- Poulain, M. *et al.*, Identification of a geographic area characterized by extreme longevity in the Sardinia island: the AKEA study, *Experimental Gerontology* **39**: 1423–1429, 2004.
- Francaalacci, P. *et al.*, Low-pass DNA sequencing of 1200 Sardinians reconstructs European Y-chromosome phylogeny, *Science* **341**:565–569, 2013.
- Sanford, J.C. *et al.*, Using computer simulation to understand mutation accumulation dynamics and genetic load; in: Shi, Y. *et al.* (Eds.), ICCS, 2007, Part II, LNCS 4488, Springer-Verlag, Berlin, pp. 386–392, 2007.
- Sanford, J.C. *et al.*, Selection threshold severely constrains capture of beneficial mutations; in: Marks, R.J. III *et al.* (Eds.), *Biological Information: New Perspectives*, Cornell University, New York, pp. 264–297, 2013.
- Jeffreys, A.J. *et al.*, Recombination regulator PRDM9 influences the instability of its own coding sequence in humans, *Proc. Natl. Acad. Sci. (USA)* **110**(2):600–605, 2013.
- Hinch, A.G. *et al.*, The landscape of recombination in African Americans, *Nature* **476**:170–177, 2011.
- Contact: us@creation.info.

**Robert Carter** received his Bachelor of Science in Applied Biology from the Georgia Institute of Technology in 1992 and his Ph.D. in Coral Reef Ecology from the University of Miami in 2003. He has studied the genetics of fluorescent proteins in corals and sea anemones and holds one patent on a particular fluorescent protein gene. His current research involves looking for genetic patterns in the human genome and the development of a biblical model of human genetic history. He works as a speaker and scientist at CMI-US.

**Matthew Powell** is a computer scientist and entrepreneur currently residing in Colorado, USA and is married with 4 children. He studied Computer Science, Mathematics and Philosophy at the University of Western Australia and completed a Bachelor of Computer Science and Mathematics. He worked in the field of Data and Information Science for SAS Institute and Nokia and holds a number of patents in the field of mobile software and digital security. More recently, Matthew founded a number of successful software startups in Australia and the USA and has become increasingly passionate about Creationism, specifically the intersection of Biology and Information Science.

# Young evidences in an ancient landscape: part 2—high-altitude sapping

*Kenneth H. Karle*

Pronounced erosional features consistent with formation by ground water sapping were mapped in a 25,000-km<sup>2</sup> section of the sedimentary Ridge and Valley area of the Appalachian Mountains in Pennsylvania. These features were evaluated by criteria known to cause hydraulic sapping—a natural erosional process initiated by water levels receding after complete inundation of sediment. Over 600 saps were mapped and carefully measured, revealing easily identifiable features known to be caused by ground water sapping. Supposedly very old, these saps exhibited distinct topographic forms, geometry, location, elevation, and profile. The sap formations studied reside at a high elevation in relation to the ridge they formed under—some even existing on either side of the same ridge at the highest possible elevation. Sufficient ground water to create saps would not be expected at these elevations. The study area was never glaciated, ruling out formation by impounded melt water. The traditional theory, that millions of years of erosion acting on the originally ‘Himalayan’-sized Appalachians reduced them to their present size, cannot explain these distinct and repetitive structures. These saps are better explained as recent formations created by the recessional stage of a catastrophic inundation.

**E**rosion by sapping is caused by focused ground water discharge from the lower side of a saturated embankment of sediment.<sup>1</sup> During the discharge process, sediment is removed along with the water. Completely submersed sediments have all interstitial spaces occupied by water, retarding compaction and lithification (diagenesis).<sup>2</sup> As the inundating water elevation lowers, the unconsolidated sediment particles are carried out at the low side of the now emerging shoreline by seeping action of the entrained water. This erodes the hillside from underneath, undermining the overlaying layer, which slumps into the lower discharge of water,<sup>3</sup> carrying the sediment away. The process continues until the entrained water at the higher elevations in the emerging sedimentary hillside has mostly discharged.

Examples of sapping can be found in the southwest United States where lack of vegetation, extensive sandstone landscapes, and limited rainfall make ground water saps easier to observe. The Escalante River basin in Utah is a good illustration of this phenomenon (figure 1). The lack of vegetation from limited rainfall in a sandstone landscape encourages the formation of undercutting on the lower slopes with minimal evidence of upslope runoff gullies or drainage basins. Steve Austin has postulated that this may be one mechanism that formed the side canyons of the Grand Canyon,<sup>4</sup> as these canyons are characterised by short lateral distance, no head end gullies, under-fit (or no) streams or seeps, and are amphitheatre headed.

Sediment tank experiments have demonstrated that the sapping process starts with random breakouts of water occurring at areas of weakness in the saturated sediment. As the seeps develop, the minor erosion causes a slight

deflection and concentration of ground water discharge<sup>5</sup> from the surrounding sediment by providing a shortened path of escape. Erosion into the hill creates easier paths of escape for adjoining seeps, causing the area of erosion to progress not only into the hillside, but laterally to the left and right as well. This causes the distinguishing ‘amphitheatre headed’ characteristic of saps,<sup>6</sup> resulting in bowl-shaped depressions that often have ratios of length to width near 1:1. It also explains why there are no head end (inlet) streams, and why there are no drainage basins. The erosion is from below and from within—not from the top down.

When first forming, new saps consume each other along the seepage line, resulting in lateral lines of saps with fairly uniform spacing and similar sizes (figure 2). The process is self-defining, creating recognisable patterns, which are the focus of this paper.

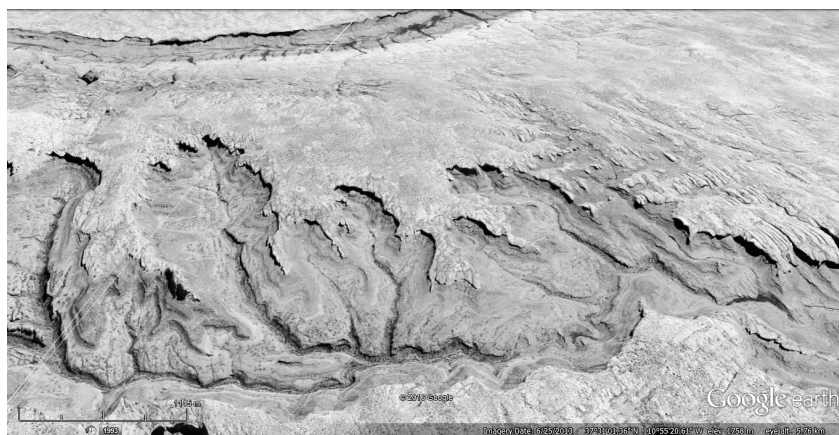
To summarise, saps are unique erosional features formed by:

- dropping water elevation
- seepage (sapping) of non-cemented saturated sediment
- erosion from underneath, not from surface run-off.

Saps can be identified by:

- no inlet water course
- no outlet water course except for intermittent streams during heavy precipitation or occasional springs
- a bowl shape (amphitheatre headed)
- a distinct discharge point or throat
- side-by-side alignment along similar elevation at regular intervals.





**Figure 1.** Sap formation in the Escalante River Basin in Utah, US (Google Earth Pro, image date 25 June 2013, generated 2 April 2016)

### Study area and its lithology

For this study we carefully mapped features that appeared to be the result of hydraulic sapping in the 25,000-km<sup>2</sup> area of the sedimentary Ridge and Valley Province<sup>7</sup> of the Appalachian Mountains in Pennsylvania. The ridges are formed from resistant quartzitic sandstone underlain by mudrocks and carbonates.<sup>8</sup> The area was not glaciated<sup>9</sup> and recent geologic processes are not attributed to this area.

The Ridge and Valley Province is comprised of systemic units ranging from Cambrian to Pennsylvanian, and especially Silurian and Ordovician,<sup>10</sup> meaning none of the area is thought to be younger than 290 Ma old.

The folded strata forming the ridges are generally comprised of Silurian red and grey sandstone, conglomerate, shale, and limestone overlain on lower Ordovician shale, limestone, dolomite, and sandstone.<sup>11</sup> The lower Silurian deposits consist of rippled sandstone, channel-fill sandstone, planar-bedded or parallel-laminated sandstone, and other combinations of sandstone and shale deposited cyclicly.<sup>12</sup> Upper Silurian strata shift to limestones and dolomites.<sup>13</sup> Sand-sized sediment favourable for sap formation is present in abundance.

### Methodology

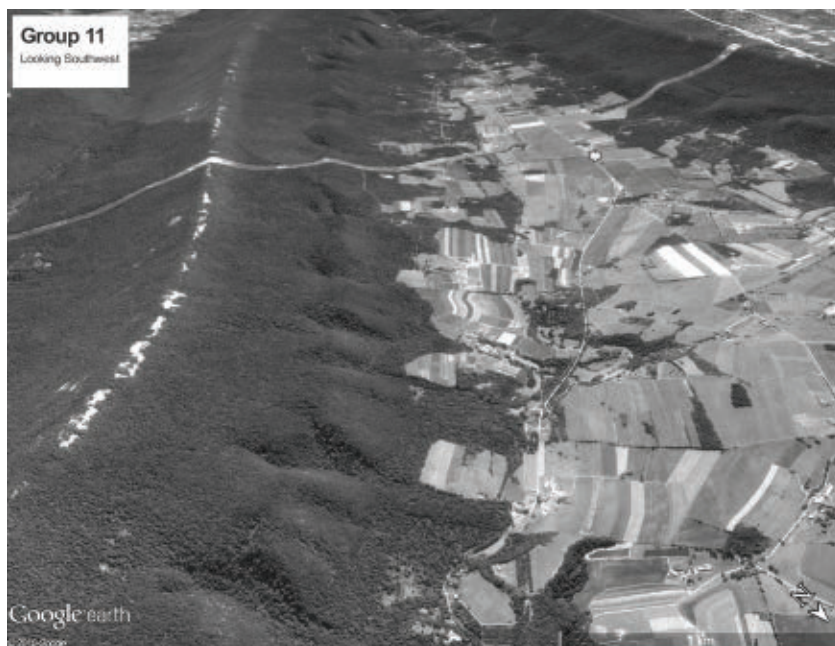
Identification and measurement of each suspected sap was accomplished using commercially available topographical mapping software.<sup>14</sup> We

did not map low altitude saps or the sapping features east of the Susquehanna River in the anthracite coal region. We did identify saps in this area, but they were less numerous and are the subject of further research.

Figure 3 demonstrates how each sap was tagged with a label, mapped and measured. The drainage basin contributory to each sapping formation was overdrawn with a polygon traced at right angles to the topographic contour lines. We did not include the area below the throat discharge of the sap, but used the adjoining ‘knobs’ at either side of the sap as a self-defining lower limit of

the drainage basin mapping. Most of the structures were easy to delineate. The mapping software automatically tagged each drainage basin polygon with the perimeter and area uphill of each sap.

A dimension line was then drawn across the widest part of the lower side of each sap connecting the high point of each knob to determine its width. This line was also used as a section line to draw a profile across the throat and calculate the lowest elevation along this line. We defined



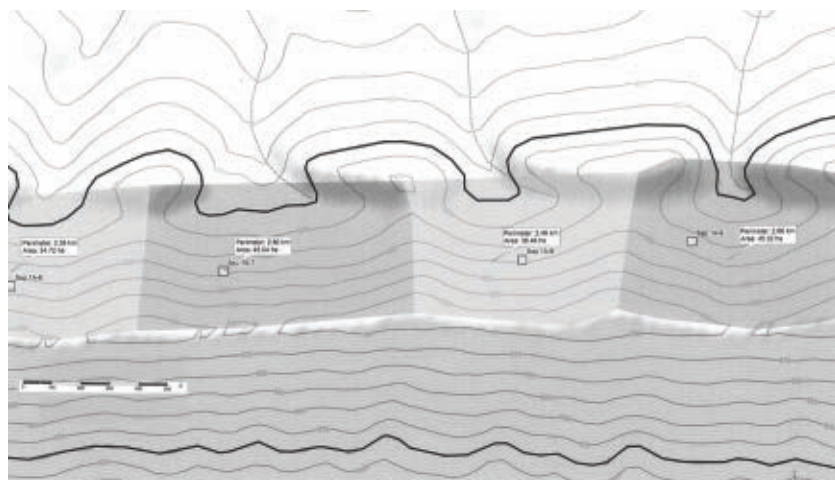
**Figure 2.** A line of saps in Group 11 looking southwest. Note the even spacing and linear arrangement of the saps along the same elevation. There are no inlet streams or downslope discharge streams. The ridge on the left is marked by an unvegetated outcrop of resistant rock. The sediment filled, relatively flat valley in the centre is marked by farmland (landsat source image generated three dimensionally by Google Earth Pro on 23 May 2015).

and recorded this as the ‘Invert at Throat’. This technique provided a consistent methodology for establishing a ‘discharge’ elevation from the sap.

The highest elevation of the ridge above the sap was recorded. The highest area eroded by the sap and the lowest area eroded below the throat discharge were also recorded. These last two measurements required considerable interpretation of the contour lines and are subject to an accuracy of  $\pm 20$  m at best. The most difficult observation was the elevation of lowest influence caused by each sap because there were occasional gullies or valleys extending well down the slope from either original or modern run-off. However, many saps did have a recognisable lower limit to their influence on the surrounding topography—an indication that they stopped forming and are relic landforms. Further, an accuracy of  $\pm 1$  m for ridge elevation and width of the sap,  $\pm 10$  m for ridge sag and  $\pm 0.01$  km<sup>2</sup> for drainage area, was maintained.

### Types of saps

The saps occur in several general forms. The classic amphitheatre-headed sap confined by elevated landmasses or ‘knobs’ at one or both sides of the discharge area was called ‘Type 1’. The saps that had no knobs, but otherwise maintained most of the other features just discussed, were called ‘Type 2’ (figure 4). We did not try to map every Type 2 sap because there is a point where they become indistinguishable from surface erosional features. We did map Type 2 saps where they were intermingled with the predominant Type 1 saps or where they were arranged linearly because of the higher certainty that they were true



**Figure 3.** A relief map of typical saps studied. The drainage areas are shaded, perimeter and area measurements are added and the 550 m contour line is highlighted on either side of the ridge (image derived from Delorme Topo USA 8.0 software, 25 m contour interval, overdrawn by author).

saps and not surface erosion. The measurements of the less-defined forms of Type 2 saps are less reliable.

We infrequently observed some saps that were elongated (T-shaped) or contained double bowls. We called these ‘Type 3’ and ‘Type 4’ respectively. These were not found in great number. We felt it was appropriate to record these occasional formations when grouped with Type 1 saps even though they are outliers to the classic shape.

We also excluded any saps located well below the ridge line, usually at an elevation below 400 m ASL (above sea level) because of the general nature of stream beds, plains, and general erosion prevalent below this elevation that made detailed mapping difficult. There are clearly some lines of ‘low altitude’ saps that exist at the base of the mountains, but they are not the topic of this paper.

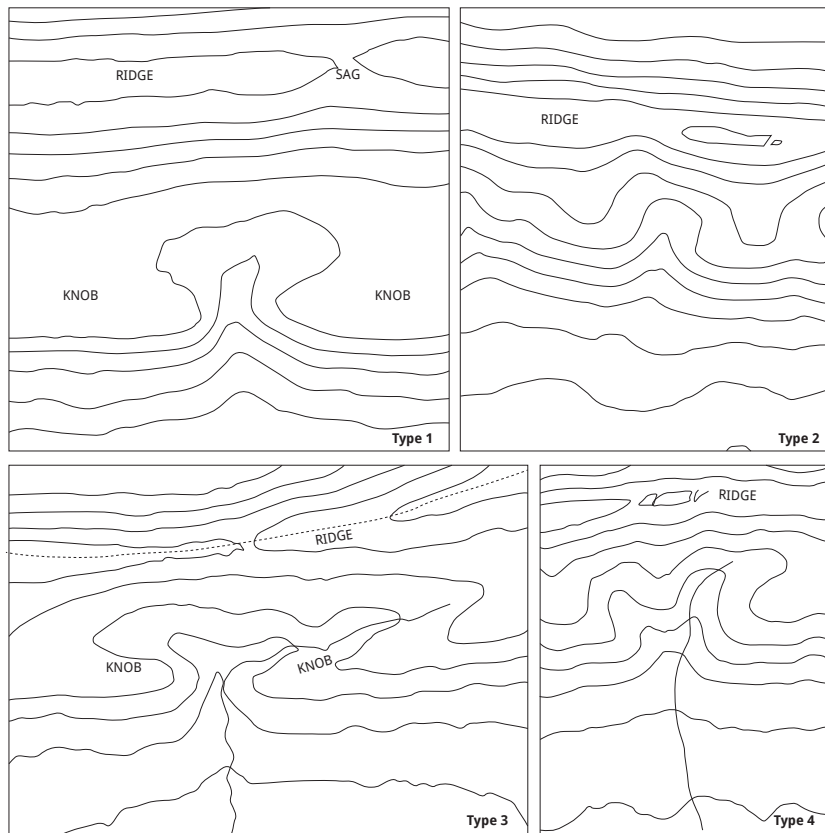
### Observational bias

Many saps were well defined and could be readily identified and measured. Others required subjective evaluation. To eliminate as much observational bias as possible, we used the following procedures:

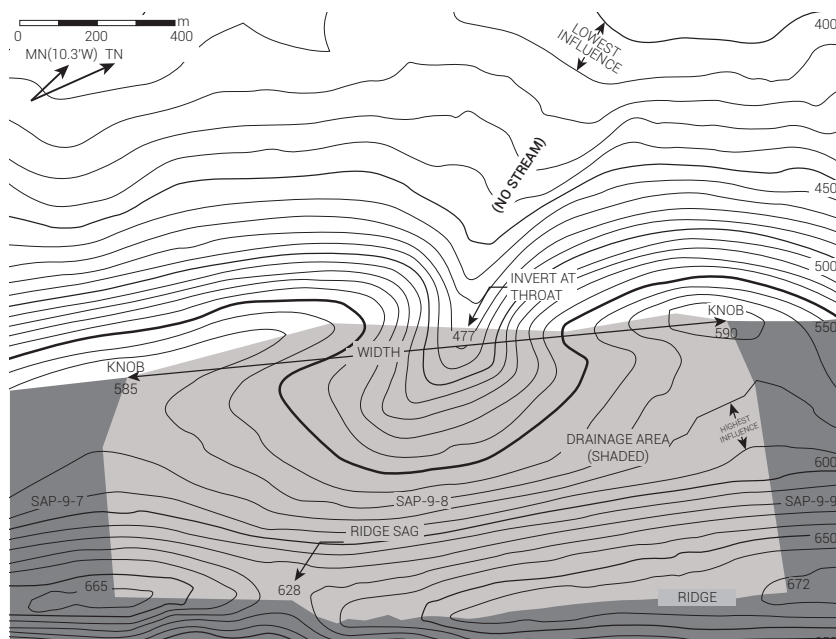
- Identification: after a first pass through the study area, we went back and systematically scanned from west to east along grid lines from north to south at a high zoom factor<sup>15</sup> and preliminarily marked each suspected sap. This zoomed-in study of 15–45 km<sup>2</sup> areas removed our ability to see regional patterns. It also revealed many smaller saps that cannot be seen at larger scales. Hundreds of well-defined saps were less than 1 km<sup>2</sup> in total drainage area.
- Non-inclusion: during the identification process, we identified hundreds of other possible saps we did not include in our study. Many of these appeared to be partially formed without enough characteristic features to accurately measure. Some could have been caused by surface run-off. Some long linear Type 3 saps followed double-ridge structures with active streams and geometry far removed from the ‘classic’ Type 1 saps. We did include Type 3 saps that were not obviously controlled by long streams. We intentionally did not include low-altitude saps occurring just above the adjoining valley floors.
- Measurement: several ‘self-defining’ measurement techniques were established to quantify each sap:

**Drainage basin area:** we mapped the full contributory area above each





**Figure 4.** General shapes of Type 1, 2, 3, and 4 saps (image derived from Delorme Topo USA 8.0 software, 25 m contour interval, labelled by author).



**Figure 5.** A relief map of a typical sap (Sap #8 in Group 9) used to illustrate how measurements were taken. Elevations are in metres above sea level and the 550 m contour is highlighted (image derived from Delorme Topo USA 8.0 software, overdrawn by Matt Fink).

feature from the throat of the sap all the way up to the ridge line, even though some saps did not extend all the way to the ridge line. Almost all the saps are bounded on either side by the next sap, so this technique gives an absolute maximum of drainage area available to influence the formation of the sap by surface or ground water.

**Sap width:** we used a line drawn from the highest point of each knob of Type 1 saps to determine width. This allowed a consistent and self-defining point of geometry to be used for measurement, even though the sap discharge continued well below this line. Type 2 saps could not be measured in this manner, making the measurement of their widths and inverts much more subjective.

**Throat invert:** we used the same width measurement line to generate a profile across the discharge throat of the sap. The mapping software automatically calculated the lowest elevation along this line, which was recorded as the invert of the sap throat even though the sap discharge valley continued well below this line.

- **Ridge sag:** the upper extent of the drainage basin often aligned with a sag in the ridge (discussed in detail later). This was not obvious until the drainage basin contributory to each sap was delineated with a polygon (figures 3 and 5). This mapping revealed a strong correlation between ridge sags and saps in more than half of the saps.

- **Naming:** many of the saps near populated areas were named, such as ‘Black Gap’ or ‘Bear Gap’. We did not use this as a method to locate saps, but it confirmed that they are identifiable features with enough prominence to have been named.<sup>16</sup>

## Observations

Figure 6 maps the location of each sap for which we obtained measurements. We were able to identify 379 Type 1 sapping structures,



**Table 1.** Average sap measurements by type

Description	Throat Invert (m ASL)	Ridge Sag (m)	Ridge Height (m ASL)	Highest Influence (m ASL)	Lowest Influence (m ASL)	Area (km <sup>2</sup> )	Width (km)	Ratio of Area to Width (km <sup>2</sup> /km)
All Type 1 saps	430.13	8.13	625.42	515.20	319.95	1.21	1.31	0.93
Type 1 saps with no stream	432.43	5.87	613.93	504.18	340.61	0.86	1.05	0.82
All Type 2 saps	483.62	7.51	646.00	549.98	394.40	0.49	0.71	0.69
All Type 3 & 4 saps	420.59	15.52	620.45	521.03	292.07	2.06	2.56	0.80
Saps with stream	411.66	12.31	627.72	523.01	268.71	2.27	2.21	1.02
Saps with Intermittent stream	449.13	10.00	647.08	537.66	326.88	1.05	1.22	0.86
Saps with no stream	456.18	6.52	626.96	523.85	369.67	0.67	0.88	0.76
All saps	447.68	8.27	632.11	527.18	343.69	1.01	1.17	0.87

**Table 2.** Sap quantities by drainage area

Drainage Area of Sap (km <sup>2</sup> )	Quantity of Saps	Quantity of Saps with Permanent Stream	%
1.0 or less	427	18	4.2%
1.01–2.0	109	32	29.4%
2.01–3.0	41	18	43.9%
3.01–4.0	26	13	50.0%
More than 4.0	12	12	100.0%

and these occurred on both sides of ridges and throughout the study area.

We calculated the ratio of area to width, confirming that many of the saps were near the ratio of 1 km<sup>2</sup> in area by 1 km wide—that is, bowl shaped. The average ratio was 0.87 km<sup>2</sup>/km with only 10 saps less than 0.3 km<sup>2</sup>/km and only 11 saps more than 2.0 km<sup>2</sup>/km. We used this calculation only to look for outliers and to test that the saps were not linear drainage features. Although there appear to be some outliers in the data, their effect on the analyses was not large enough to warrant excluding any of the raw data collected.

We grouped the saps with similar characteristics and averaged the measurements to produce table 1. Table 1 confirms that saps with a stream have the lowest average throat invert and the lowest average influence below the sap. We expected this because of modern erosion and assumed we would need to exclude saps with active streams from our analysis. However, the erosion was not great enough to significantly alter the averages, and saps with permanent or intermittent streams were not excluded. This suggests that the ongoing down-cutting erosion by streams has not been occurring long enough to significantly alter the shape and elevation of the saps. If the saps were ancient relics,

modern streams in the larger ones should have deepened or elongated them, destroying their distinctive form.

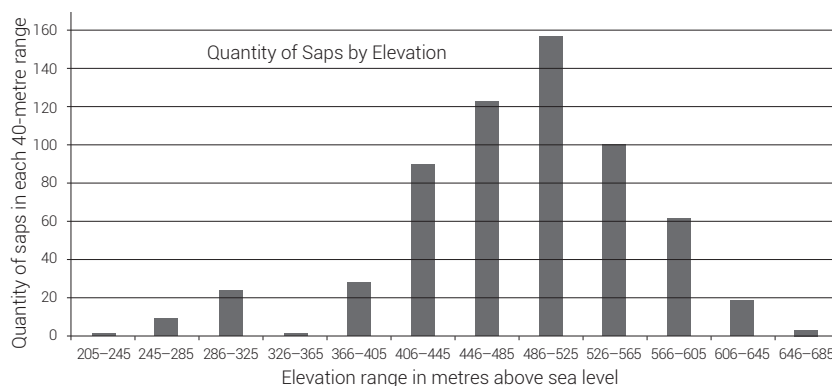
We further analysed the effect of modern streams on the saps in table 2. The majority of the saps, which are the smallest saps, have few permanent streams, attesting to the fact that streams are not what formed the saps. All of the saps greater than 4 km<sup>2</sup> have a catchment area large enough

to support permanent streams from precipitation—enabling modern erosion. However, only 2% of the saps studied are this large.

During mapping, there appeared to be a bias of sap formation near elevation 500–550 m ASL. 72% of the saps had at least part of the structure at or above 500 m ASL. Saps grow downward as the sapping spring carries sediment away and they also grow upward as the headwall collapses. To arrive at an approximate starting elevation, the throat invert and the area of highest influence were averaged and the result used to produce figure 7, which graphs the quantity of saps by elevation in 40-metre increments. 80% of the saps were in the range of 402–570 m ASL, peaking at 486–525 m. Figure 7 demonstrates that the saps do have a preferred elevation for formation. The saps disappear below 366 m except for those forming just above the valley floors. There is a ‘dead band’ of no formation between 325 and 365 m. This preferred elevation for formation occurs in distinct ridges spread over 25,000 km<sup>2</sup>, negating the possibility that uniform geology caused the elevation preference. The well-defined inverted ‘V’ shape of figure 7 is suggestive that a force that can arrange erosional features horizontally over vast distances, such as floodwater, would be a better explanation for the sap locations, rather than random erosion.



**Figure 6.** Map of the 25,000 sq km study area. The white squares label the centre of each group of saps. The black triangles are drawn to scale over each individual sap measured (image derived from Delorme Topo USA 8.0 software, overdrawn by author).



**Figure 7.** The quantity of saps grouped by elevation

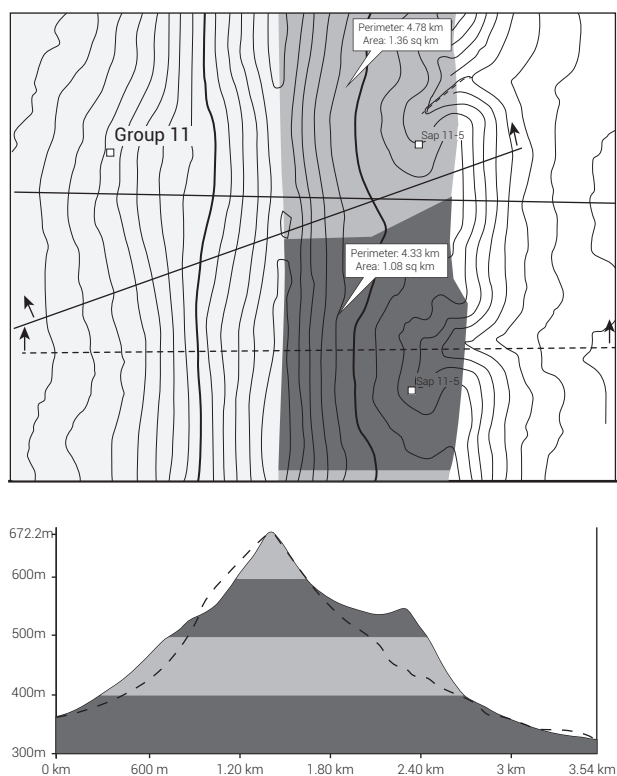
The west edge of the Ridge and Valley Province is marked by a structural front (figure 6). North and west of the structural front, the geomorphology changes to an elevated rolling topography with a dendritic drainage pattern, mostly above 550 m. This landmass would backstop the elevated sea level of the recently opened Atlantic Ocean to the south and east.

### Ridge sag

An unexpected observation developed as each sap was mapped. The uphill extent of the drainage basin often aligned exactly with heightened points on the ridge above the sap at both the right and left edge of the drainage basin (figures 3, 5 and parts of figure 4). A sag in the ridge was only recorded if the ridge elevation was lower somewhere along the ridge line of the contributory drainage area than at the ends. If the ridge was sloping overall from one edge to the other, it was not counted as ridge sag. The amount of sag in the ridge was measured in 10-m increments to identify that it did exist, rather than to try to quantify it in absolute terms. 57.7% of the saps correlated with a sag in the ridge. This raised the question of whether the sap formation caused the ridge to sag or whether another mechanism was at work, such as overtopping of the ridge by waves or tsunamic action, especially where the ridge sags were in the 20–50 m range forming more of a ‘gap’ than ‘sag’. The observation is quantifiable regardless of the mechanism that caused it.

### Benched profiles

A second unanticipated finding was that the saps did not cut into the side of the mountain slope. Rather, they cut through a ‘bench’ on the side of the slopes. This is best illustrated by cross sections cut through the saps to



**Figure 8.** The upper topographical map shows where sections were cut. The 550-m ASL contour line is highlighted. The lower profiles drawn through the sap (dashed line) and through the knob (solid line) demonstrate that the saps follow the overall slope of the mountain while the area between the saps stands prominently above the expected slope (vertical exaggeration 4:1). (Images derived from Delorme Topo USA 8.0 software, overdrawn by author.)

demonstrate the effect. Figure 8 shows a typical condition where saps formed on only one side of a ridge in a raised area or ‘bench’ in the profile.

Assuming that resistant strata caused the ridge to form, a back-sloped area could result along a secondary outcrop of resistant strata further down the slope, feeding surface runoff into the saps. Dispelling that possibility, figure 9 shows a typical condition where saps formed on *opposite sides of the same ridge at the same elevation*.

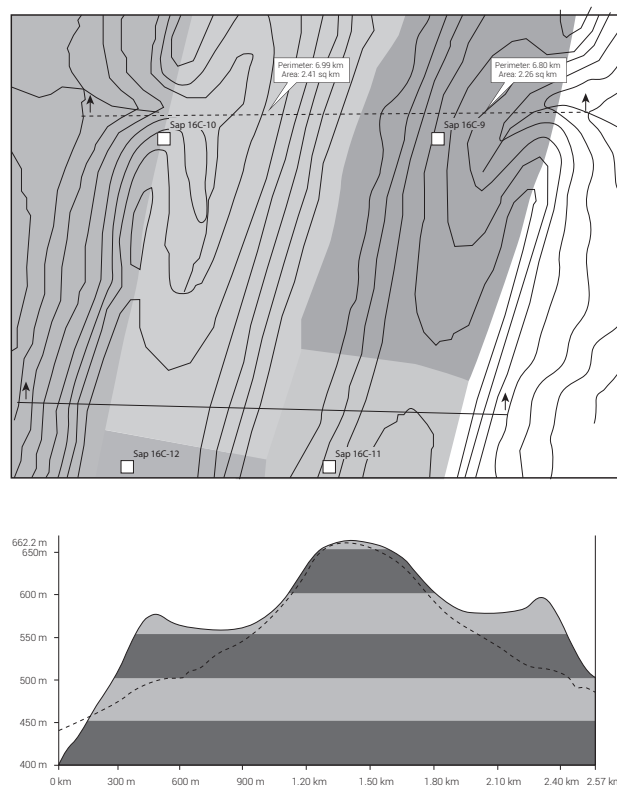
Receding tides can create similar benched profiles on a smaller scale (figure 10). A receding tide with gentle wave action produced the same profile in miniature as that observed in the Appalachians (compare figure 10 with figure 2). The constant slope is interrupted by a bench that then develops knobs flanking each sap.

Figure 11 demonstrates how wave action may be a formative part of the sapping features studied. A lower sloped benched area (relative to the overall beach slope) is formed during the receding tide, possibly by shore parallel currents. The receding tide initiates sapping action. The

deepening sap areas capture the waves, diverting energy away from the knobs. The knobs survive above the surrounding topography and help funnel the erosive wave energy into the saps, reinforcing the sap formation with distinctive knobs. The scale of figure 11 is diminutive, but the resulting formations demonstrate that sapping reinforced by wave action on a receding tide can produce the distinctive formations recorded in Pennsylvania.

## Discussion

For reasons discussed above, the level of 500–550 m ASL can be used as a present-day marker indicative of a rapid lowering of sea level. Below 550 m ASL, the ridges of the Ridge and Valley Province started to act as linear islands in the receding sea, changing sheet flow into channelised flow forced to run parallel to the ridges as water level dropped. Landforms indicative of the transition from sheet flow to channelised flow were also postulated just below 500 m ASL in the previously published Part 1 of this paper, based on other criteria.<sup>17</sup>



**Figure 9.** Similar to figure 8, profiles drawn through the saps (dashed line) and through the knob (solid line) where saps occur on both sides of the same ridge at the same elevation suggest formation controlled by elevation rather than formation controlled by underlying structural geology (erosion-resistant strata) (Vertical exaggeration 4:1). (Images derived from Delorme Topo USA 8.0 software, overdrawn by author.)





**Figure 10.** A small-scale example of a receding tide producing landforms in loose sediment, similar to those observed in Pennsylvania. The pronounced knobs, nearly equally spaced, formed in several hours by a combination of hydraulic sapping and gentle wave action (Lovers Key State Park, west coast of Florida at the Gulf of Mexico). (Photo by author.)



**Figure 11.** A demonstration of how wave action may be a formative part of the sapping features studied. The deepening sap areas capture the waves diverting energy away from the knobs. The entire cycle only lasts for a fraction of one 6-hour receding tide yet leaves a distinctive landform (Lovers Key State Park, west coast of Florida at the Gulf of Mexico) (Photo by author).

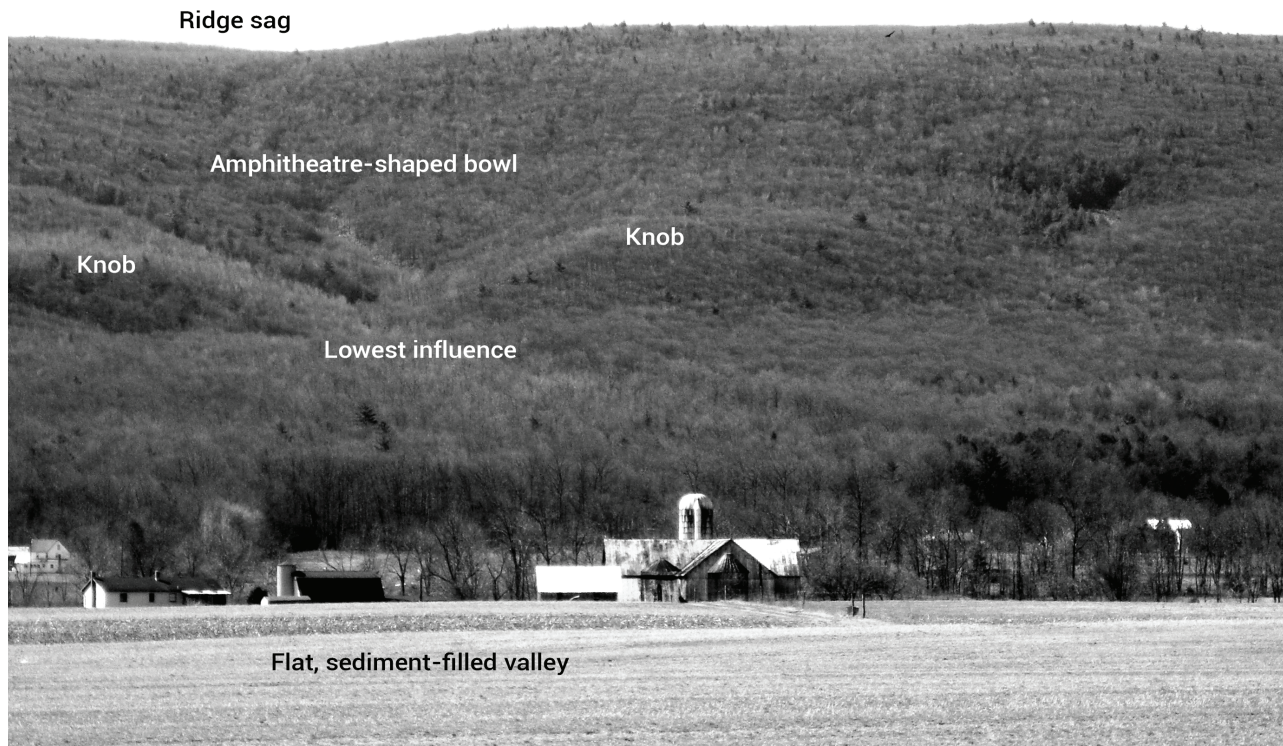
The averaged height where the sap discharges become generally indistinguishable from the surrounding topography was 343.7 m ASL. We calculated this measurement as a possible location where sea level lowering paused—terminating the sapping action. A sea level residing for a time slightly below 343 m ASL would remove the sapped sediments and could also leave traces of a remnant shoreline if not too much time passes (figure 12) (as discussed above, this is a fairly subjective measurement and is not able to be recorded where streams have formed permanent valleys). Part 1 of this paper, published in 2009, calculated a similar change in slope at the bottom of the Eastern Structural front southwest of the Susquehanna River Water Gap (i.e. this study area) of 342.5 m ASL<sup>18</sup> and published two figures showing accumulated scree along a line of this same general elevation at and near the Delaware River Water Gap, further to the east.<sup>19</sup>

## Conclusion

A distinctive landform repeats hundreds of times in the Appalachian Mountains of Pennsylvania. These landforms are characterised by distinct features postulated to be the result of hydraulic sapping, such as bowl-shaped canyons, no head stream, distinctive profiles, and a narrow range of area-to-width ratios. Careful measurements were analysed to demonstrate the consistency and distinctiveness of the 615 saps studied. Two other distinct features uncovered by this study—aligned sagging in the ridge and distinctive knob formations flanking the discharge throat—may be the result of wave action interacting with sapping action.

The saps formed at high elevations just below or flanking the ridges and are arranged in linear groups. These high elevations (in relation to the





**Figure 12.** A typical Type 1 sap formation exhibiting knobs on either side of the amphitheatre-shaped bowl below a corresponding sag in the ridge. (Note the farm buildings and silos for scale.) The sap formation ends well above the valley floor with no discharge water course and no accumulated outwash delta or scree. Similar formations repeat regularly to the right and left of the photo at the same elevation parallel to the flat valley floor. A receding inundation could have created the conditions needed for horizontally arranged sap formation and sediment transport (Photo by author).

ridge above) do not provide an adequate ground water reservoir to sustain prolonged sapping, although they may be saturated intermittently.

Slope profiles with benched areas along consistent elevations were associated with many of the saps even though some of the saps are separated by up to 200 km.

The long held teaching that these ridges are remnants of Himalayan-size mountains subjected to millions of years of erosion cannot explain these distinctive and consistent features. High altitude hydraulic sapping can be explained by recession of flood waters from still consolidating sediment after total inundation of the more than 25,000 km<sup>2</sup> area studied. The fact that the saps have recognisable topographic footprints and profiles is testimony to relatively recent formation; otherwise their distinctiveness would have eroded away.

The recessive stage of the flood, in Genesis 8:1–14, records the scenario that may have produced the high-altitude hydraulic sapping still visible today. The biblical chronology explains the unique conditions needed to form these features in a timeframe of months during a rapidly lowering sea level less than 5,000 years ago.

### Definition of terms

- Definitions of terms used in this paper are as below (and illustrated in figure 5):
- Drainage area: the total extent of the current landform that can contribute surface run-off above the throat of the sap, always measured to the ridge.
- Highest influence: the approximate location at the top of the amphitheatre where the contour lines change from a circular pattern to a mostly straight pattern parallel with the ridge.
- Invert: the lowest water-carrying point of any drainage structure at a defined point. In this case, the invert is measured at the lowest elevation of the throat at the point where the section line drawn between knobs crosses the throat.
- Knob: the generally circular area of elevated landmass flanking the throat of Type 1 saps. Water will flow off all sides of a knob, even back toward the hillside. Knobs are indicated by closed circle contour lines.
- Lowest influence: the approximate location below the throat discharge where the 'V'-shaped contour lines (normally indicative of a stream channel) change to generally straight lines.

- No stream: defined by the mapping software with the lack of a solid or dashed blue line.
- Ridge sag: A low point in the ridge above the sap. The ridge line across the top of the sap drainage area must be higher at two locations compared to any point in-between. Multiple sags are included. Ridges that decline in elevation from one side to the other are not considered ridge sag. Some Type 1 saps exhibit exact alignment of the two high-end points of the ridge with the knobs flanking the sap throat.
- Throat: the point of drainage discharge from the bottom of the sap. Most throats are now dry, but may convey an intermittent stream or permanent stream if the sap has a spring or is large enough to collect precipitation.
- Width: the width of the sap as measured from the peak of one knob to the other. In Type 1 saps this measurement is self-defining. In Type 2 saps the width is measured subjectively from the approximate widest point of the drainage area at the low side passing across the throat.
- Bench: a lower sloped area on a higher sloped mountainside suggesting formation by a change in the initial erosion mechanism. Saps were found to form in the benches.
- Group #: an arbitrary number assigned to each group of saps for general identification purposes only. The group numbers are generally arranged in three arcs from southwest to northeast. There is no significance to the 'A', 'B', 'C', etc. after the number.
- High altitude: the relative location of the sap compared to the ridge. For this paper it means the highest areas of influence of the sap amphitheatres are averaging more than 500 m above sea level in ridges averaging 632 m above sea level.
- Intermittent stream: defined by the mapping software with a dashed blue line.
- Sap #: the saps in each group are numbered consecutively, always from southwest to northeast (left to right). Saps in the figures are identified by combining the Group # and the Sap # with a dash, such as 16A-3 (the third sap from the southwest or left in Group 16A).
- Stream: defined by the mapping software with a solid blue line.

## References

1. Rosenberry, D., *Ground-water sapping and the generation of natural amphitheatres*, Geography Department, University of Colorado, Boulder, CO., Geological Survey, [www.colorado.edu/geography/geomorph/geog6241/GWsapping.htm](http://www.colorado.edu/geography/geomorph/geog6241/GWsapping.htm), accessed 16 June 2015.
2. Imperial College Rock Library, Glossary: Diagenesis, [wwwf.imperial.ac.uk](http://wwwf.imperial.ac.uk), accessed 16 June 2015.
3. Luo, W., Quantifying groundwater-sapping landforms with a hypsometric technique, *J. Geophysical Research* **105**(E1):1686, 2000.
4. Austin, S., *Grand Canyon: Monument to Catastrophe*, Institute for Creation Research, Santee, CA, pp. 6, 99, 100 and 254, 1994.
5. Rosenberry, D., referencing diagram by Dunne, T., Formation and Controls of channel networks, *Progress in Physical Geography* **4**:211–239, 1980.
6. Luo, ref. 3, p. 1685.
7. Faill, R.T. and Nickelsen, R.P., Structural geology and tectonics—Appalachian Mountain section of the Ridge and Valley Province; in: Shultz, C.H. (Ed.), *The Geology of Pennsylvania*, The Pennsylvania Geology Survey, Harrisburg, PA, and The Pittsburgh Geological Society, Pittsburgh, PA, p. 269, 2002.
8. Schultz, C.H. (Ed.), *The Geology of Pennsylvania*, The Pennsylvania Geology Survey, Harrisburg, PA, and The Pittsburgh Geological Society, Pittsburgh, PA, p. 14, 2002.
9. Crowl, G.H. and Sevon, W.D., Quaternary; in: Shultz, C.H. (Ed.), *The Geology of Pennsylvania*, The Pennsylvania Geology Survey, Harrisburg, PA, and The Pittsburgh Geological Society, Pittsburgh, PA, Fig. 15-2, p. 226, 2002.
10. Faill and Nickelsen, ref. 7, Figure 19-1, p. 268.
11. Schultz, ref. 8, inside cover.
12. Laughrey, C.D., Silurian and Transition to Devonian; in: Shultz, C.H. (Ed.), *The Geology of Pennsylvania*, The Pennsylvania Geology Survey, Harrisburg, PA, and The Pittsburgh Geological Society, Pittsburgh, PA, fig. 6–9, p. 97, 2002.
13. Laughrey, ref. 12, p. 91.
14. TOPO USA, Version 8, DeLorme Publishing.
15. Zoom factors 12 and 13, TOPO USA, Version 8, DeLorme Publishing.
16. Many of the names end with the term 'gap' even though these are not gaps, but saps. Gaps form a cut through the ridge; saps do not, although more than half of the saps were associated with a 'sag' in the adjoining ridge. There are many other true gaps in Pennsylvania also carrying names, but gaps were not mapped in this paper.
17. Karle, K., Young evidences in an ancient landscape: part 1—the Eastern Structural Front of the Appalachian Mountains, *J. Creation* **23**(3):82, 2009.
18. Karle, ref. 17, table 1, p. 77.
19. Karle, ref. 17, figures 2 and 4, p. 78.

**Kenneth H. Karle** has a B.Sc. (Hons) degree in Architecture from the Pennsylvania State University. He is both a Registered Architect and Professional Engineer in the states of New Jersey and New York, U.S.A. He serves as president of an 80 person architecture and engineering firm designing schools, public buildings and similar projects.



# Thinking correctly about science

Martin Tampier

Dutch philosopher Herman Dooyeweerd (1894–1977) has made a major contribution towards a Christian theory of reality (ontology). Next to using scientific evidence to show that evolutionary mechanisms proposed today cannot account for the emergence of life-forms from abiotic matter and the existence of increasingly complex life-forms, Dooyeweerd's approach is a second, philosophical method creationists can use to support Genesis as a historical account.

## Dooyeweerd's approach

In his theory, Dooyeweerd proposes that we understand creation as having multiple aspects, where an 'aspect' is defined as "a basic kind of properties and laws". Examples of such kinds are: mathematical, spatial, physical, biotic, sensory, logical, linguistic, and ethical (in all, he distinguishes 15 such aspects of created reality). He argues that all these aspects are exhibited by reality, i.e. they are mutually irreducible both in the sense that none can coherently be eliminated in favour of another and also that none can be coherently regarded as the cause of any other.

The core idea is that all aspects are created, since there is nothing that God did not create (Isa. 44:24; John 1:3; Eph. 3:9; powers and principalities: Rom. 13:1; Col. 1:16; space: Rom. 8:38; time: Tit. 1:2; 2 Tim. 1:9; Rev. 10:6; all visible and invisible things: Col. 1:15). This includes matter and life, the laws of logic, and the laws governing all the other aspects (Jer. 31:35; 33:25). The theory goes on to argue that all things in creation have (active or passive) properties of every one of the aspects and so are subject to the laws of all the aspects.

The aspectual laws apply to things in two different ways, however. Things can have properties either actively or passively. For example, a rock has a specific physical weight whether we know its weight or not. It has this property independently of an observer. But its sensory colour is not independent. Rather, it only appears black in relation to a perceiver. What the rock has actively (independently of us) is the disposition to appear black. That potentiality is actualized only when it comes into relation with the activity of perception. Thus the rock's colour is a passive property because it requires being acted upon by a perceiver in order to be actualized. That is, although a rock cannot actively perceive it can passively be perceived and that ability is a (passive) sensory property of the rock.

A chart of these aspects is offered in table 1 but more explanation is required to describe the theory. First, it takes note of the observed fact that, as far as we know, only human beings have active properties in all 15 aspects. Second, the first six (lower) aspects on the chart are governed by laws

that cannot be broken (for example, the physical law of gravity determines how fast a stone falls to the ground). By contrast, the higher ones are ordered by norms and can be violated. Norms therefore show us how things ought to be, rather than guaranteeing what will take place. Third, the aspects as listed in table 1 reflect Dooyeweerd's argument that the aspects lower on the list (earlier in the cosmic order of aspects) are preconditions for aspects higher on the list, but that no aspect produces any other.

For example, it is necessary for there to be things with active physical properties in order for there to be things with active biotic properties, which are in turn necessary for there to be things that have active sensory properties.

## What is 'divine'?

Elaborating on Dooyeweerd's ontology in the book *The Myth of Religious Neutrality*, Roy Clouser explains why one does not have to be a follower of any religion to be genuinely religious. Whereas religious teachings differ as to what (or who) is divine, Clouser shows that all known religions agree on what it means to be 'divine'. In every tradition, the divine is understood as the self-existent reality on which all else depends for existence. So, on this definition even atheistic materialists are religious since they postulate some purely physical reality said to be self-existent as the cause of everything that is not self-existent. Far from having no divinity belief whatever, they simply have a different idea of the divine. Instead of worshiping the Creator, they replace God with something created (Rom. 1:25), in this case matter.

A further consequence of this definition is that it shows how religious beliefs can be tacitly assumed by theories of science, so that science itself is not religiously neutral. As Clouser puts it:

"... scientific theories necessarily presuppose a view of the nature of reality, while such overviews of reality necessarily presuppose some per se divinity belief. Religious belief thus regulates overviews of reality directly, and through the mediation of some overview regulates scientific theories indirectly."<sup>1</sup>

Thus, from a Christian point of view, regarding any aspect of the natural world as having divine (that is, independent) reality, leads to the reduction of the remaining aspects to the one regarded as divine. In this way, belief in a false divinity leads to an erroneous interpretation of scientific data.<sup>2</sup>

In this way the Bible's claims that all knowledge is hidden in Christ (Luke 11:52, Rom. 1:28, 1 Cor. 1:15, Col. 2:3) take on new meaning. These verses are not based on some arcane body of mysterious lore, but on an understanding of our world in such a way that none of its aspects are reduced to any other. It means rescuing the sciences from the deleterious effects of reductionist ontologies. In other words, pagan ontologies assume that the universe or some part of it is self-existent and thus divine. A Christian<sup>3</sup> ontology, on the other hand, presupposes that all things, along with their properties and laws, depend on an outside and independent cause, i.e. God who called them all into existence and continues to sustain them in existence (Heb. 1:3, 11:3, 1 Cor. 8:6). So whereas naturalist theorists try to show that all the aspects of reality reduce to the one or two it has selected as divine (usually, the physical aspect), the Christian approach should be thoroughly non-reductionist. From a Christian viewpoint,

no properties or laws found in creation are to be regarded as self-existent since God has created "all things visible or invisible" (Col. 1:16). But neither should Christians allow that anything of creation mediates between God and the rest of creation. It is not that God created, say, matter/energy and the rest of creation depends on that. Thus, not only is nothing in the cosmos self-existent, but nothing in the cosmos is what everything else in the cosmos depends on. Rather, Christians should take the position that everything in creation is *directly* sustained by God since Col. 1:17 specifically says that only Christ mediates God's power to creation.<sup>4</sup> Dooyeweerd's ontology thus rejects even the weakest senses of reduction in favour of the view that that no one aspect is the cause of any of the others. In his ontology, all aspects are equally dependent on God, equally real, and mutually irreducible.<sup>5</sup>

### Implications for evolutionary thought

As per table 1, there is a step change from each aspect to the next: something is either limited (actively) to the physical or is also alive,<sup>6</sup> it has sensory or analytical abilities or does not, exists in dimensional space or does not. If evolution were true, things with biologically active properties would

**Table 1.** A biblically informed perspective on creational diversity as opposed to an emergent view that tries to accommodate evolutionistic ideas

Aspects	Biblical view	Emergent view	Entities*
Fiduciary Ethical Justicial Aesthetical Economic Social Linguistic Historical Logical	Created by God at the beginning. Distinct laws created for each aspect. New/higher active aspect functions provided for in a special creative act to make human beings.	Things active in these aspects emerged gradually from things active in lower aspects but only in 'recent' evolutionary history. Problem to explain new phenomena that are non-material (e.g. mind, consciousness) based on physical or biotic properties.	Humans
Sensory Biotic	Only life begets life. Steady degradation and loss (devolution) of genetic information since creation, as observed in fossil record, DNA damage, subspecies formation with less genetic breadth of information, etc. Life created as variable 'kinds' that cannot develop new features as observed in the fossil record (stasis: a toad will always father more toads, but never anything else).	The first living organism emerges by chance from abiotic material. Mutation and selection over billions of years brings about new life-forms (the exact mechanism to bring about new genetic information in DNA is unknown). Kinds/species are not constant over time.	Animals Plants
Physical	Created by God.	Emerges from big bang. Physical laws created by God.	Matter
Kinematic Spatial Quantitative	Created by God.	God causes big bang to occur. Laws created by God.	Matter

\* Called 'things' in the text, using a philosophical term encompassing all created things.

have to have emerged from things that were previously active only in the lower aspects.<sup>7</sup> Likewise, things operating actively in the highest aspects must be an epiphenomenon of biological life.

Since reality is defined by distinct aspects and aspect-specific laws, there must be boundaries between these aspects that cannot be bridged or else we could not clearly distinguish any aspect. If things with new active properties can emerge from lower towards higher aspects then transitional forms of things should exist not only with respect to the evolutionary tree of life but also for any other aspectual transition. Based only on observation, there is no reason to postulate the emergence of life from physically qualified things unless one *already* believes an evolutionary process accounts for life on Earth. Rather, both the modal aspects and the things qualified by each are observed to be distinct and without transitions from one to the next.

Evolutionary concepts face the difficulty of explaining the gradual emergence of active properties in things from one aspect to the next, and even qualitatively different properties within the same aspect (e.g. the emergence of male and female within the biotic aspect). To try and overcome this difficulty, a subgroup of theistic evolutionists originating with German theologian Bernhard Bavink (1879–1947) accepts the initial creation of all things by God but posits that things ‘emerged’ from one aspect into the next higher one, including the emergence of life from the physical (a concept called ‘emergent evolution’).<sup>8</sup> Dooyeweerd himself was skeptical of this idea, writing that life is: “an irreducible modality of our experiential horizon, which cannot be defined by secondary phenomenal criteria. The philosophical theory of emergent evolution does not explain anything when it assumes that life is an emergent evolutionary result of dead matter.”<sup>9</sup>

### Teleology and emergent evolution

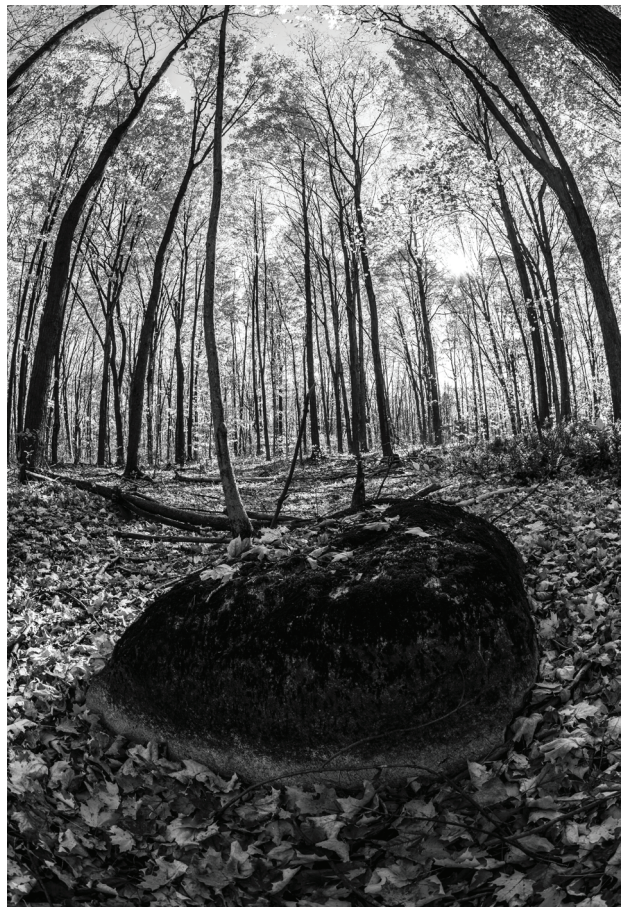
Atheist philosopher Thomas Nagel of New York University claims in his book *Mind and Cosmos* (2012) that consciousness is microscopically embedded in matter as proto-mental properties, such that they can then ‘emerge’ in an evolutionary process. So, rather than claiming that mental properties such as consciousness are reserved for higher beings, Nagel proposes that such properties already exist in matter in principle (a theory called panpsychism) but can only be expressed or realized once organisms exist that are complex enough to function actively in this area.

Such a view, if correct, would eliminate the hard, distinct boundaries between things qualified by different ontic aspects: we could no longer clearly distinguish life from non-life since proto-biotic and mental properties would be embedded in seemingly lifeless matter and in theory, dead

matter could become alive at any point in time since it supposedly has done so in the past. Secondly, we are right to ask what a proto-mental property is and how we can know that such a thing exists. Why assume mental properties in something when there is no consciousness? It seems there are more questions than answers in this approach.

But Nagel needs a second element to explain mind and reason, i.e. a tendency in the universe to evolve in the ‘right’ direction that seems as if the universe had a mind of its own (called teleology) directed at bringing about complex life-forms, rather than staying sterile. French molecular biologist Jacques Monod (1910–1976), also an atheist, made this astonishing claim about emergent evolution in his famous book, *Chance and Necessity*: in his opinion, given enough time, life necessarily *had to* appear. He believed that the possibility of life emerging by itself from matter was something that was ‘built into’ the universe from the very beginning.

Instead of acknowledging a Creator who creates purposefully, matter now becomes even more divine than



**Figure 1.** Evolutionists need to go to lengths in trying to explain complex phenomena, such as consciousness—up to suggesting that some proto-mental properties exists in stones, for example (photo by Martin Tampier).



explained above, taking on will-like properties. Yet, the universe around us only suggests that forces are at work which work powerfully *against* the emergence of life: radiation destroys complex molecules, oxygen neutralizes them, extreme hot and cold, and the great majority of the universe is extremely hostile to it. Even once life exists, no teleological drive can be observed: “The simultaneous co-existence of the greatest variety of life forms, from amoeba to humans, anyway proves that from the perspective of nature these are all equitable and equally viable, without any necessity of further development.”<sup>10</sup> This is confirmed by (evolutionist) anthropologist Gould:

“I believe that the most knowledgeable students of life’s history have always sensed the failure of the fossil record to supply the most desired ingredient of Western comfort: a clear signal of progress measured as some form of steadily increasing complexity for life as a whole through time. The basic evidence cannot support such a view, for simple forms still predominate in most environments, as they always have. Faced with this undeniable fact, supporters of progress (that is, nearly all of us throughout the history of evolutionary thought) have shifted criteria and ended up grasping at straws.”<sup>11</sup>

Whence, then, comes the idea of teleology? And even if Nagel were right in attributing mental properties to all matter, how would such properties account not only for consciousness but also for the manifold other step changes throughout the supposed evolutionary history (formation of the DNA code and reading apparatus, movement, multicellular life, male and female, feeling, speech, etc.)? Can proto-mental properties account for all these new phenomena, or would it be necessary to postulate that all higher properties already exist as proto-properties (not just passive properties in Dooyeweerd’s sense) in matter?

Dooyeweerd’s ontology clearly speaks against what Nagel is suggesting. The same objection can be made with respect to emergent evolution (as a matter of fact, Dooyeweerd linked Bavink’s emergent evolutionism to panpsychism<sup>12</sup>). Explaining the mechanism of emergent evolution requires reconciling both the distinctness and irreducibility of modal aspects while at the same time holding that biotic or other higher properties can be explained based on what happens at the level of lower aspects. As Nagel himself observes, this is particularly objectionable with respect to the appearance of completely new things, such as an immaterial mind, from qualitatively different things, such as physically or even biologically qualified things.

Christian philosopher Jacob Klapwijk, in his book *Purpose in the Living World?*, nevertheless tries to reconcile evolution with the biblical account, likewise adding teleology to the neo-Darwinistic mechanism, which is purely based

on chance mutations and selection. Based on an interview<sup>13</sup> about the book, the author makes the following assertions:

1. There are clearly distinguishable, distinct ‘domains’ of things, such as the physical (matter), the biotic domain of unicellular life, the vegetative domain (plants), the sensory (animals), and the mental (mankind).
2. Genetic similarities between algae and plants and between chimpanzees and humans show they are the fruit of an evolutionary tree of life.
3. New qualities that can be observed in each realm have emerged as life became more complex, not as a foreseeable process such as when crystals form when water freezes but as new laws and principles that become active as a new domain emerges over time.

Yet, he is unable to make a case other than by circular reasoning, as one reviewer summarizes: “Evolution has produced a complex interlacing and organic system where the emergence of mind and awareness of logical connections is itself the evidence of purposeful development.”<sup>14</sup> In other words, Klapwijk presupposes evolution as fact and then takes the complexity of life as evidence for a directed evolutionary process because random mutations and selection alone cannot explain it. Moreover, he draws conclusions such as point two, above, that do not follow from the premise, since genetic similarities do not prove common ancestry, also being fully compatible with and expected in a special creation scenario.<sup>15</sup>

Moreover, he believes that subparts of living organisms, such as DNA, came into existence by chance and then took on new, life-like properties such that biotic modal laws could then apply to them, bringing forth new active properties (“conglomerates of physical particles came into the grip of new modal laws, laws of life”).<sup>16</sup> Almost magically, such previously physically qualified particles would then have started to obey higher biotic laws of DNA replication etc.

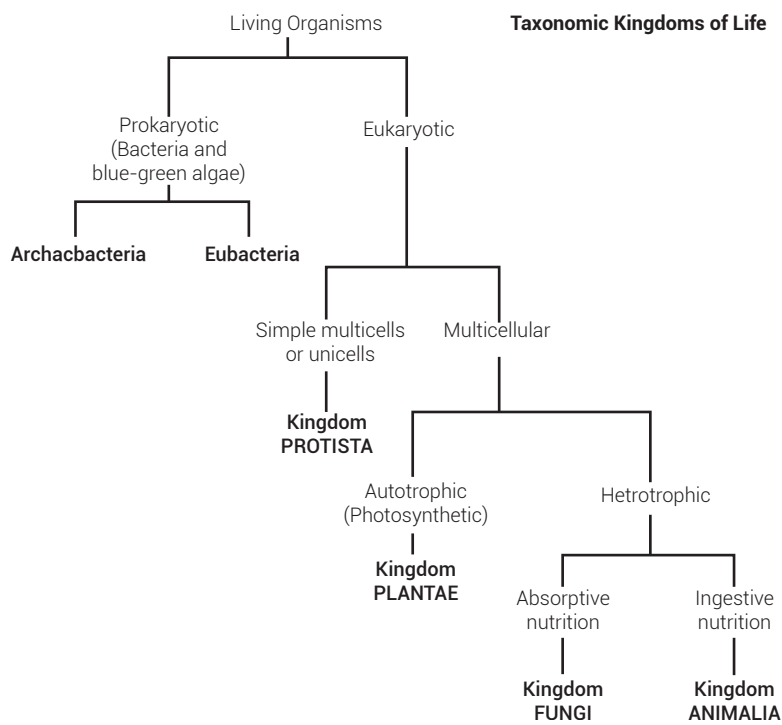
The problem with this reasoning is, however, that DNA by itself is identical to the remains of decaying life: the existence of DNA makes no sense apart from a complete, living organism. Experience tells us that molecules cannot self-organize themselves into systems; the total, functional system is required to organize the molecules via downward causation. So, DNA does not reconstitute itself with other molecules into life as in spontaneous generation—if this were possible, it would mean that scientists could reproduce such a process in a test tube but until today, nobody has proven Louis Pasteur wrong in his finding that “only life begets life”.

Realizing that mere materialism and the Darwinistic mechanisms of mutation and natural selection are insufficient, the ideas sketched out above try to add another ‘mechanism’ to explain how ‘evolution plus ...’ could have brought about the biosphere we see today. As historian Peter Bowler (1944–) points out, none of these ideas are new: emergent evolution has already been proposed by

philosophers about a hundred years ago to explain the sudden appearance of completely new properties at different stages of an evolutionary process.<sup>17</sup> In 1907, French philosopher Henri Bergson came up with the idea of the ‘*élan vital*’, a life force that works in lifeless matter, pushing it towards the formation of living entities. Psychologist C. Lloyd Morgan, like Nagel today, held in 1922 that mental properties were present in matter, such that evolutionary processes could then lead to the emergence of the mind over



**Figure 2.** Emergent evolutionary concepts fail to explain step-changes observed in nature, such as the appearance of an ability to fly (photo by Martin Tampier).



**Figure 3.** The existence of distinct kingdoms of living things denies the notion of evolutionary transition between different life forms.

time without miraculous divine intervention to bring this about. The entire process of evolution was directed towards the emergence of man, and this direction came from God.

Panpsychism puts this directing mechanism *inside* matter, i.e. matter is driven towards the emergence of life by some proto-life qualities, which ‘seek’ expression in living organisms that can sense and think logically. This view is rejected in Dooyeweerd’s ontology, which does not allow for active properties to exist—even embryonically—outside a modal aspect the laws of which apply to them (for example, only things qualified by the biotic or higher aspects feature active biological features, but not things qualified by lower aspects).

On the other hand, emergent evolution posits a mechanism that is *outside* matter: next-level aspectual laws that define and control things with new ontic qualities take over (as in pulling the thing up to a higher level of being) when a thing crosses aspectual boundaries (“satisfies essential conditions for further development”, as Klapwijk words it).

Yet, it remains a mystery how a) things can satisfy essential conditions (a term that demands the pre-existence of laws to qualify ‘essential’) spontaneously and b) laws of a higher aspect can cause new active properties in a thing hitherto qualified by a lower aspect. As Geertsema put it, such a thing “would be at the same time the result of emergence and its condition”.<sup>18</sup>

Driven by this difficulty of emergent evolution, Clouser posits God-given overarching natural laws (he calls them emergence laws), which guide evolutionary processes from dead matter towards the emergence of man.<sup>19</sup> The existence of emergence laws<sup>20</sup> would mean, by analogy, that just because we draw up procedures as to how a car should be assembled and function, the car would then auto-assemble itself through natural processes without any further input. Such laws cannot be shown to exist through scientific enquiry (laboratory experiments). Just like the idea of biological evolution itself,<sup>21</sup> they must remain speculative.<sup>22</sup> They therefore do have no apparent advantage over other ‘*Deus ex machina*’ arguments that call upon divine intervention to stop any gaps left by evolutionary explanations. In addition, they deny that we can ever know which theory of origins is true—a most unsatisfactory position to take.

In theistic evolution, God is supposed to have guided the evolutionary process such that the emergence of life from matter

would occur, and intervened miraculously at the emergence of mankind and other key transitional points. The idea of emergence laws invokes God again to have guided evolutionary processes—not through either continuous or miraculous ad-hoc interventions but by aspect-transcending laws that existed from the beginning of the universe. These unknown laws must work against known natural thermodynamic laws, to bring about complex life out of lifeless matter. In addition, it appears they are no longer active today since we do not observe the emergence of new life-forms from abiotic material or any other transitions of things from one aspect level to the next.

## Conclusion

The distinctness of modal aspects is anchored in our experience with all created things: from a molecule over algae and mammals to humans, each kingdom features new active properties that do not exist in the lower kingdoms, neither do they exist—nor can be imagined—as transitional properties. A philosophy that presupposes a loving God who has given us the ability to observe, know, and experience the world in a meaningful way necessarily leads us to trust our observations. The distinctness and irreducibility of modal aspects and laws tells us, then, that things could not have ‘emerged’ or evolved from each other, having their origin in God and without the means of some evolutionary process that cannot account for the step changes in the properties we observe. Accepting the uniqueness of created things in combination with a limited degree of genetic variability, on the other hand, provides a wholesome and non-contradictory explanation as to why different things display entirely different active properties. It follows that the logical outcome of a Christian worldview is to reject evolution as an explanation for the emergence of living things. The main reason special creation is rejected as the best explanation for origins is a pre-existing bias towards physicalistic evolutionary explanations.

## References

1. Clouser, R.A., *The Myth of Religious Neutrality—An Essay on the Hidden Role of Religious Belief in Theories*, University of Notre Dame Press, Notre Dame, IL, p. 78, 2005. (I am indebted to Roy Clouser for many helpful comments on the various drafts of this article.)
2. For example, atomic theory was invented by pagans who were trying to identify the divine material the cosmos is made of. There were theories that said it is earth, air, fire, and water. After a few centuries of debate, Democritus and Leucippus came up with the idea that there are tiny particles that combine to form earth, air, fire, and water. They thought these things (they called them “atoms” which means “that which cannot be divided”) were divine. Epicurus agreed with them, holding that all that exists is atoms in space. This does not make atomic theory false, yet because they thought of atoms as purely physical, they came to a false interpretation of atoms.
3. The term, Christian, is used here to indicate coherence with a Christian worldview. It may also be coherent with what other monotheistic religions hold.
4. Clouser, ref. 1, p. 173.
5. The theory is difficult to summarize in a few pages. A summary of Dooyeweerd’s ontology is Clouser’s essay, *A Brief Sketch of the Philosophy of Herman Dooyeweerd*.
6. One could object that viruses represent an intermediate stage between life and non-life, yet once we consider they depend on living organisms to reproduce, it becomes clear they cannot have been life’s predecessors.
7. Of course the development of an embryo and later the growing of a child to adulthood entails several emerging properties, such as speech and moral and aesthetic judgment. Yet, this is all (at least in part) governed by genetic material that already exists. To propose that this information itself also emerged in some natural process is quite another issue.
8. This requires an interpretation of Genesis as saying that the material world ‘brought forth’ life by itself (e.g. “let the earth bring forth” or “let the sea bring forth”), despite the text clearly stating that God made specific animals and man (Gen. 1:21,25,27).
9. Dooyeweerd, H., *A New Critique of Theoretical Thought*, vol. III. Padeia Press Ltd, Jordan Station, Canada, p. 84, footnote 1, 1984.
10. Eisenstein, I., Ist die Evolutionstheorie wissenschaftlich begründet?; in: *Philosophia Naturalis*, Archiv für Naturphilosophie und die philosophischen Grenzgebiete der exakten Wissenschaften und Wissenschaftsgeschichte, vol.15, no.3, Part 1, 1975. English translation quoted from Strauss, D., *Philosophy: Discipline of Disciplines*, Padeia Press, Grand Rapids, MI, p. 484, 2009.
11. Gould, S.J., *Life’s Grandeur*, Vintage, Random House, London pp. 166-167, 1996.
12. Gould, ref. 11, p. 645, footnote 1.
13. Wetenschap weet niet wat zonde is, *Nederlands Dagblad*, 29 May 2009.
14. Ewart, P., *Purpose in the living world?* (review), *Science & Christian Belief* 22(2):189.
15. See creation.com/human-chimp-dna-similarity-re-evaluated; creation.com/is-the-evolutionary-tree-changing-into-a-creationist-orchard.
16. Creation Belief and the Paradigm of Emergent Evolution, *Philosophia Reformata* 76:20, 2011.
17. Bowler, P., *Reconciling Science and Religion: The Debate in Early-Twentieth-Century Britain*, University of Chicago Press, Chicago, IL, pp. 136, 2001.
18. Geertsema, H., Emergent Evolution? Klapwijk and Dooyeweerd, *Philosophia Reformata* 76:50–76, 2011.
19. Despite the thrust of this article based on his book, Prof. Clouser favours belief in a type of theistic evolution, i.e. the emergence of life from matter based on natural processes. He reconciles Dooyeweerd’s ontology of distinct aspects by assuming God also created “inter-aspectual bridge laws” that enable a transition (evolution) from lower to higher aspects of reality (although he does not cite any such laws in his material). It should also be mentioned that Dooyeweerd himself was uncertain with respect to the creation/evolution debate; he believed that man can never understand how God created in detail, i.e. whether through evolutionary or other means. This article therefore goes beyond what the author of the discussed ontology himself thought.
20. Emergence laws have been proposed by philosophers many decades ago. They would be a statement of the irreducible fact that an aggregate composed of aggregates of the next lower order in such and such proportions and arrangements has such and such characteristic and non-deducible properties. (see: utsc.utoronto.ca/~seager/pan\_seager.pdf)
21. See creation.com/refuting-evolution-2-chapter-3-argument-evolution-is-true-science-not-just-a-theory.
22. Indeed, Jacob Klapwijk, a proponent of emergence, admits that “a causal explanation is lacking” and that “one cannot expect a well-worked-out answer to this problem from science” (see *Creation Belief*).

**Martin Tampier** is a professional engineer and energy consultant in Laval, Quebec (Canada). He is writing on various elements of the Christian life, including creationism, culture, and other Bible related topics.



# Instructions to Authors

**JOURNAL OF CREATION** is dedicated to upholding the authority of the 66 books of the Bible, especially in the area of origins. All our editors adhere to the Creation Ministries International (CMI) Statement of Faith and most papers will be designed to support this. Rarely, other papers may be accepted for publication on merit so that certain issues can be clarified. The views expressed in the papers are those of the authors and not necessarily those of CMI.

Because the scope of this journal is broad, we welcome articles on any topic that is relevant to biblical creation. This includes the sciences such as geology, chemistry, biology, astronomy, etc., and also archaeology, theology, hermeneutics, biblical history, geography, linguistics, ethics and society, philosophy, law, etc. Potential authors should familiarise themselves with the journal and its position and style before submitting articles. Authors should also indicate if their manuscript has been submitted elsewhere, address previous articles on the topic, and ensure the work of others is properly acknowledged.

**Word length:** Shorter articles are more likely to be read so preference will be given to publishing them. All articles, including letters, may be edited for brevity and clarity. Perspectives: 1,000–2,000 words; Book reviews: 1,500–3,000 words, but please enquire first. You may be asked to scan the cover of the book; Letters to the editor: 1,000 words. We will publish critical letters on articles already published, but a reply will usually follow the criticism; Papers, Overviews, Countering the Critics, Viewpoints and Essays: <5,000 words.

Articles must be written clearly and concisely and should be focused on only one topic/subject. The most readable articles are those with an average sentence length of about 17 words, with one idea per sentence. Do not use too many big or extra words such as “in spite of the fact that” when “although” would do. Please use first person sparingly and do not use “this present writer”, which is verbose false modesty and ambiguous. Care with spelling is crucial, and British spelling generally applies. Personal invective or similar comments against others are not acceptable.

Specialist technical terms and abbreviations should be defined the first time they are used. If many technical terms are used, these should be included in a glossary. SI units should be used in scientific papers. Words in non-Latin alphabets (e.g. Hebrew, Greek and Russian) must use Unicode characters and be accompanied by a transliteration, also in Unicode characters (Unicode should avoid errors when the file is transferred to a publishing program or HTML).

**Abstract:** All articles except Perspectives, Letters and Book Reviews should be preceded by an Abstract, which should not exceed 200 words and must be without abbreviations and reference citations. The Abstract should summarise the key points of the paper and be comprehensible to readers before they have read the paper.

**References** should be indicated in the main text by superscript numbers in sequence and then listed in numerical order at the end of the text (End Notes). Full details of all references are required, including all authors and their initials, the full title of the paper or book, the full title of the journal or its accepted abbreviation, the volume number, the page number(s), the editor(s) of the book or proceedings (if applicable), the publishers and place of publication (in the case of a book), and the year of publication. If a citation is repeated, then the same superscript number should be used (a cross reference).

**Quotes** must be verbatim, with omissions clearly shown by ellipsis (...). Even erroneous grammar and spelling in the original must be reproduced, and indicated by [sic]. Any additions or explanations within a quote need to be placed in square brackets []. Primary sources are preferred, but if a secondary source must be used, the reference format must be [primary source], as cited in [secondary source]. For internet URLs the date last downloaded should be included.

**Tables** should be embedded in a Microsoft Word document, with brief, self-explanatory titles, and captions if an explanation is essential to understanding the table. Tables should be numbered according to their sequence in the text and all should be referred to in the text, e.g. (see table 1).

**Graphics** should be supplied electronically on CD or by email to [journal@creation.info](mailto:journal@creation.info) as 300dpi \*.TIF, \*.EPS, \*.PSD, \*.AI, \*.JPG, \*.PDF or \*.BMP files, not embedded into a document file. They can be sent in colour or greyscale, but will appear only in greyscale in the journal. Graphics should have a minimum size of 80 mm x 80 mm when printed (preferably 1024 x 768 pixels). Photographs are acceptable provided they have good contrast and intensity, and are submitted as sharp, glossy copies or as 35 mm slides. Computer print-outs are not acceptable.

**Figures** should be numbered according to their sequence in the text. References should be made in the text to each figure. In planning images and figures, the page format and column widths of the journal should be kept in mind and should allow for the possibility of reduction. Each illustration should have a self-explanatory caption. The captions should be collected together at the end of the article document file. If graphics are not provided with a manuscript, authors may be asked to submit suggestions and possible sources of non-restricted material.

Copyright ownership for each and every graphic must be specified and any relevant permissions and or credit requirements given in writing. If you are not the copyright owner, please supply written permission (preferably with an original signature) from the copyright owner. If you are the copyright owner, your submission of a graphic will be taken to grant us permission to use the image in the journal and also any other publications or on our website, unless you specify otherwise.

**Biography:** Papers, Overviews, Countering the Critics, Forums, Viewpoints, Research Notes and Essays should include a biography of no more than 100 words for each author. It should include the authors' qualifications and experience, and involvement in creationist work.

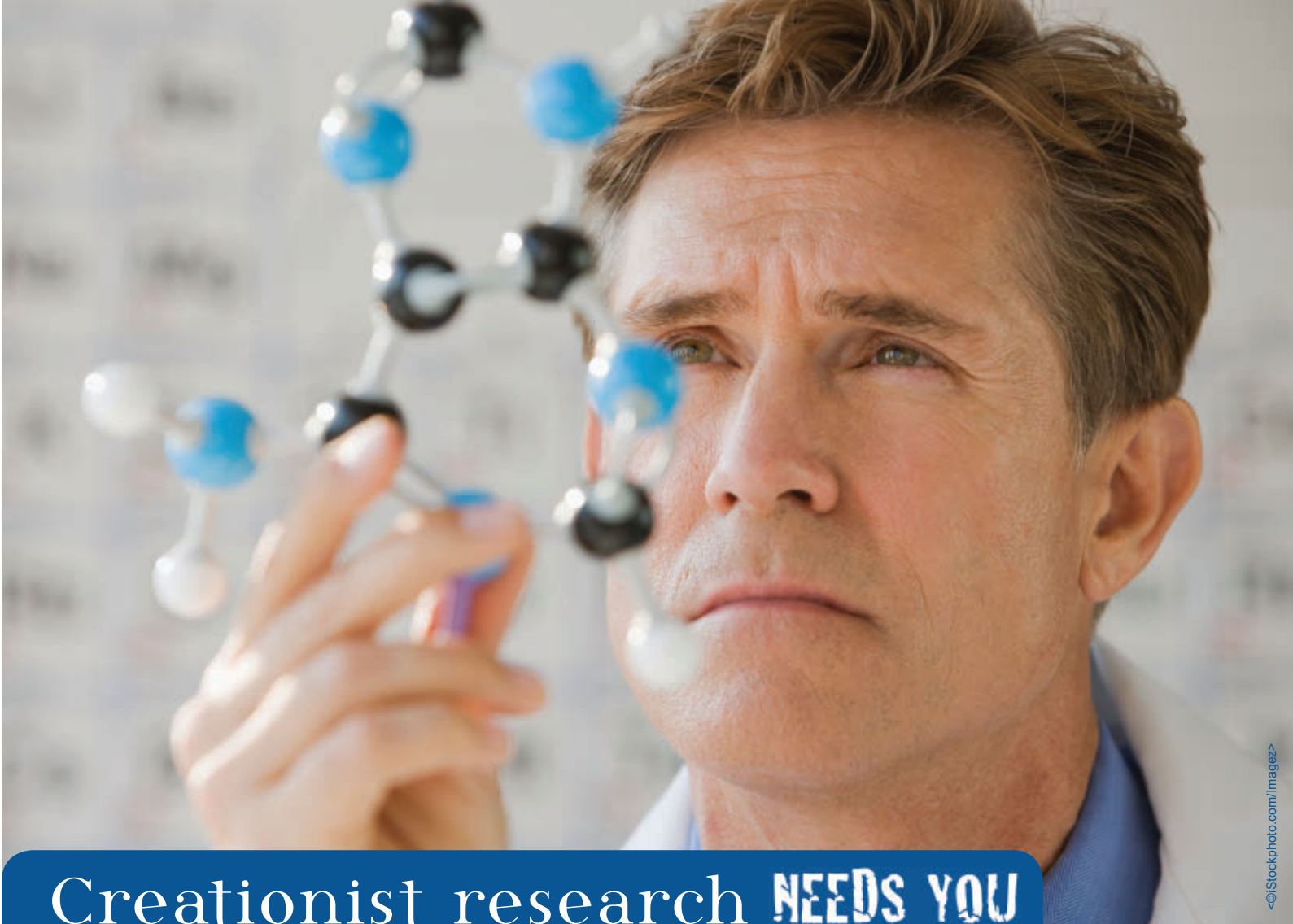
## Please also:

- send documents in Rich Text (\*.rtf) or Word (\*.doc) format, not Publisher (\*.pub) format. Excel (\*.xls) is also acceptable for complicated tables.
- type left-justified without hyphenation except for compound words
- input text continuously; only insert hard returns at the end of sections, lists, etc.
- use single spaces after each sentence within a paragraph
- use Times New Roman 10.5 font and use the word processing formatting features to indicate bold, italics, Greek, Hebrew, maths, superscript and subscript characters
- submit complex mathematical formulas or equations using MathType according to the guidelines in our “Equations layout guide”, which can be obtained by contacting us
- insert captions for graphics at the end of your manuscript
- type references in the correct order and style of the journal using the word processing “Endnotes” and “Cross-references” features to link references to the text correctly.

Photographs and/or CDs may be sent to [journal@creation.info](mailto:journal@creation.info)

The Editor,  
Journal of Creation  
Creation Ministries International  
P.O. Box 4545  
Eight Mile Plains QLD 4113  
AUSTRALIA

**NOTE: Papers prepared according to these instructions are more likely to be considered.**



<©iStockphoto.com/Imagez>

# Creationist research NEEDS YOU

**Christians need to keep on providing scientific answers within a biblical framework, and refining our case (including exposing whatever flaws there may be in old arguments). We also need to be ready to respond to challenges by critics.**

Faith-funded creationist ministries like *Creation Ministries International Ltd* (CMI) can only do so much, not having access to taxpayer dollars.

Creationist membership societies with hundreds of scientist members are encouraging by their very existence. But they are usually just as hampered by funding constraints, and would dearly love more of their members to get involved in actively helping the creationist model.

We have many qualified scientists and other educated professionals on our mailing lists, and we would like to encourage more of you to each give just a little bit of spare time to creation research issues.

## GETTING INFORMED

Start by getting as informed as possible through the existing literature. CMI can provide up-to-date catalogues.

## JOINING THE NETWORK

Consider researching a particular area with a view to producing a paper. *Journal of Creation* is a great place to air it. CMI is more than willing to provide refereeing through our contacts. If you are concerned that publishing in a creationist journal might affect your employment, for example, a pseudonym may be acceptable. If you are keen to write, see our instructions to authors opposite.

Remember that the creation/evolution issue is often not so much about *facts* as about their *interpretation*. Often the research results produced by secular institutions operating within an evolutionary framework can be just as useful in providing answers for creationists—it just needs someone to go

to the trouble of working it through. We can provide some guidance about how you can draw your research into a suitable paper.

## NO CONTRIBUTION TOO SMALL

Even producing a brief Perspective item on a specialist area, if it will teach and inform *Journal of Creation* readers, and enable them to share with others, is a worthwhile contribution.

## AND FINALLY ...

You might want to consider a donation earmarked specifically for creationist research. If so, you could direct it to any of the CMI offices listed at the front of this journal. Such donations may be tax deductible in certain countries.



THE FAMILY COMPANION TO  
**JOURNAL OF CREATION**



## CREATION magazine

IN A WORLD FLOODED WITH ANTI-CHRISTIAN MEDIA, it's nice to come home to a publication that upholds the truth of God's Word ... all the way from Genesis. Packed full of fascinating articles and beautiful full-colour photography, *Creation* appeals to both young and old.

Enjoy subjects ranging from the wonders of nature to creation/evolution, archaeology and practical Christian living.

Special children's section sure to interest your younger family members.

Join subscribers across the globe and let *Creation* magazine be your family's life-changing experience too!

// 56  
PAGES OF FULL  
COLOUR  
[NO PAID ADVERTISING]

Subscribe via **CREATION.com**, mail or phone  
(see inside front cover for contact details).

ISSN 1036-2916



9 771036 291007